

GenCore version 5.1.8
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Om protein - protein search, using SW model

Run on: May 20, 2006, 20:15:01 ; Search time 84 Seconds
(without alignments)

789.243 Million cell updates/sec

Title: US-10-705-716A-2

Perfect score: 767

Sequence: 1 MGCGGSRADAAEPRYYTSEWT..... VTEENIQRQMDRSKRKVTCIN 145

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_GeneseqD8;*

- 1: geneseqD1980s;*
- 2: geneseqD1980s;*
- 3: geneseqD2000s;*
- 4: geneseqD2001s;*
- 5: geneseqD2002s;*
- 6: geneseqD2003ab;*
- 7: geneseqD2003bs;*
- 8: geneseqD2004s;*
- 9: geneseqD2005s;*
- 10: geneseqD2006s;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	767	100.0	145	8 AD048473
2	746	97.3	145	8 AD048479
3	645	84.1	145	4 AD95018
4	645	84.1	145	5 ADQ19498
5	645	84.1	145	6 ADQ19498
6	645	84.1	145	7 ADC31800
7	645	84.1	145	7 ADG46959
8	645	84.1	145	8 ADG48475
9	617.5	80.5	180	7 ADG46961
10	473.5	61.7	149	7 ADG46963
11	335.5	43.7	92	5 ADQ19092
12	294	38.3	54	8 ADQ48481
13	288	37.5	73	7 ADM46962
14	278	36.2	54	7 ADM46960
15	278	36.2	54	8 ADG48477
16	272	35.5	80	7 ADM46964
17	140	18.3	25	7 ADM46979
18	99	12.9	18	7 ADM46977
19	92.5	12.1	778	2 ADRI13456
20	89	11.6	16	8 ADG48482
21	87.5	11.4	260	4 ABG09899
22	87.5	11.4	592	4 ABG15607
23	85.5	11.1	85.5	8 ADY09773

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_GeneseqD8;*

- 1: geneseqD1980s;*
- 2: geneseqD1980s;*
- 3: geneseqD2000s;*
- 4: geneseqD2001s;*
- 5: geneseqD2002s;*
- 6: geneseqD2003ab;*
- 7: geneseqD2003bs;*
- 8: geneseqD2004s;*
- 9: geneseqD2005s;*
- 10: geneseqD2006s;*

RESULT 1
ID AD048473 standard; protein; 145 AA.
XX
AC AD048473;
XX
DT 12-AUG-2004 (first entry)
XX
DE Rat PTH responsive gene protein.
XX
Rat PTH responsive gene protein.

PT PTH responsive gene; PAIGB; bone-forming; bone; bone density modulation; transgenic animal; osteopathic; gene therapy; osteoporosis; rat.
XX
OS Rattus sp.
XX
PN WO2004044152-A2.
XX
PD 27-MAY-2004.
XX
PR 10-NOV-2003; 2003WO-US035655.
PR 12-NOV-2002; 2002US-042553P.
XX
PA (AMHP) WYETH.
XX
PI Robinson JA, Stojanovic-Susulic V, Babij P, Murrills RJ,
XX
DR Abr5846 Human can
Abr5846 Human can
Adc31800 Human nov
Adm46959 Brain and
Ado48475 Human PTH
Ado48476 Human PTH
Adm46961 Brain and
Adm46963 Brain and
Adq81902 Human dio
Ado48481 Mous PTH
Adm46962 Brain and
Adm46960 Brain and
Ado48477 Human PTH
Adm46964 Brain and
Adm46979 Brain and
Adm46977 Brain and
Adm46975 Duryf rec
Ado48482 PTH respo
Abg09899 Novel hum
Abg15607 Novel hum
Ady09773 Plant ful

ALIGNMENTS

24	84	11.0	718	6	ABU17344 Protein e
25	84	11.0	726	6	ADAS36828 Acinetobac
26	83.5	10.9	700	5	AAB25052 Steenotrop
27	83	10.8	1433	5	ABP35624 Fungal ZB
28	82	10.7	339	6	AAE14866 S. clavul
29	81.5	10.6	600	7	ADJ70139 Human he
30	81.5	10.6	852	4	ABM40295 Human pol
31	81.5	10.6	872	4	AAM40295 Human pol
32	81.5	10.6	886	4	AAM42081 Human pol
33	81.5	10.6	886	4	AAM42082 Human pol
34	81.5	10.6	950	8	ADQ89824 Antagonis
35	81.5	10.6	974	4	AAU31506 Abal31506 Novel hum
36	80.5	10.5	275	4	ABG21379 Novel hum
37	80.5	10.5	320	8	ABG15431 Novel hum
38	80.5	10.5	1100	4	ADK73952 Plant ful
39	80.5	10.4	286	2	AAQ84930 Shrimp wh
40	79.5	10.4	AAV0097 Enterococ		Ady00097 Enterococ
41	79.5	10.4	286	5	ABP43316 B faecali
42	79.5	10.4	286	6	ABU88344 E. faecal
43	79.5	10.4	286	9	ABU13595 Enterococ
44	79.5	10.4	305	2	ADY38910 Novel Ent
45	79.5	10.4	305	2	ADY00096 Enterococ

Abu17344 Protein e
ADAS36828 Acinetobac
AAB25052 Steenotrop
ABP35624 Fungal ZB
AAE14866 S. clavul
ADJ70139 Human he
ABM40295 Human pol
AAM40295 Human pol
AAM42081 Human pol
AAM42082 Human pol
ADQ89824 Antagonis
AAU31506 Abal31506 Novel hum
ABG21379 Novel hum
ABG15431 Novel hum
ADK73952 Plant ful
AAQ84930 Shrimp wh
ADY00097 Enterococ
ABP43316 B faecali
ABU88344 E. faecal
ABU13595 Enterococ
ADY38910 Novel Ent
ADY00096 Enterococ

RESULT 1
ID AD048473 standard; protein; 145 AA.
XX
AC AD048473;
XX
DT 12-AUG-2004 (first entry)
XX
DE Rat PTH responsive gene protein.
XX
Rat PTH responsive gene protein.
XX
PT PTH responsive gene; PAIGB; bone-forming; bone; bone density modulation; transgenic animal; osteopathic; gene therapy; osteoporosis; rat.
XX
OS Rattus sp.
XX
PN WO2004044152-A2.
XX
PD 27-MAY-2004.
XX
PR 10-NOV-2003; 2003WO-US035655.
PR 12-NOV-2002; 2002US-042553P.
XX
PA (AMHP) WYETH.
XX
PI Robinson JA, Stojanovic-Susulic V, Babij P, Murrills RJ,
XX
DR Abr5846 Human can
Abr5846 Human can
Adc31800 Human nov
Adm46959 Brain and
Ado48475 Human PTH
Ado48476 Human PTH
Adm46961 Brain and
Adm46963 Brain and
Adq81902 Human dio
Ado48481 Mous PTH
Adm46962 Brain and
Adm46960 Brain and
Ado48477 Human PTH
Adm46964 Brain and
Adm46979 Brain and
Adm46977 Brain and
Adm46975 Duryf rec
Ado48482 PTH respo
Abg09899 Novel hum
Abg15607 Novel hum
Ady09773 Plant ful

The invention relates to a novel PTH responsive gene (PAIGB) fragment encoding a polypeptide. The invention further comprises: a chimeric construct comprising the isolated nucleic acid fragment operatively linked to suitable regulatory sequences; a host cell transformed with the chimeric construct; a vector comprising the nucleic acid fragment; obtaining a nucleic acid fragment encoding the polypeptide; a method for preparing a composition for diagnosing, treating or preventing bone related disorders, e.g., osteoporosis.
The invention relates to a novel PTH responsive gene (PAIGB) fragment encoding a polypeptide. The invention further comprises: a chimeric construct comprising the isolated nucleic acid fragment operatively linked to suitable regulatory sequences; a host cell transformed with the chimeric construct; a vector comprising the nucleic acid fragment; obtaining a nucleic acid fragment encoding the polypeptide; detecting the presence of the nucleic acid fragment; an antibody that specifically binds to one or more epitopes of a PAIGB polypeptide; a composition for regulating bone-forming activity in a mammal comprising the nucleic acid fragment, polypeptide or antibody

CC ; an agent that alters the expression of PAIGB gene or polypeptide;
 CC determining whether an agent alters the expression of PAIGB mRNA;
 CC screening agents for effectiveness in altering expression of the nucleic
 CC acid fragment; screening for agents useful for treating bone related
 CC disorders; evaluating the efficacy of a treatment of a bone related
 CC disorder in a subject; identifying polypeptides capable of binding to
 CC PAIGB; monitoring the effectiveness of treatment of a subject with a bone
 CC related agent; a transgenic animal comprising the DNA; an animal model
 CC for the study of bone density modulation comprising a first group of control
 CC animals; studying bone mass determinant; studying the modulation of bone
 CC mass; studying an effect of PAIGB on bone disorders; identifying an agent which
 CC has bone forming activity; and a stably transfected cell line comprising
 CC two constructs, the first construct comprising a ligand binding domain
 CC linked to a DNA binding domain which is linked to an activation domain
 CC all of which expression is driven by a constitutive promoter, the second
 CC construct comprising multiple copies of DNA binding elements linked to a
 CC minimal promoter which is linked to PAIGB cDNA, where upon the addition
 CC of chemical inducer, transcription of PAIGB gene is induced. The PAIGB
 CC polynucleotide has osteopathic activity. The PTH responsive gene may be
 CC used to treat disorders by gene therapy. The nucleic acid is useful in
 CC preparing a composition for diagnosing, treating or preventing bone
 CC related disorders, e.g., osteoporosis. This sequence represents a PTH
 CC responsive gene protein of the invention.

SQ Sequence 145 AA;

Query Match

100.0%; Score 767; DB 8; Length 145;
 Best Local Similarity 100.0%; Pred. No. 4; ge-76; Mismatches 0; Indels 0; Gaps 0;

Matches 145; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 1 MGCGGSRADAIPTPRYYESTWETESTWLTYTDSDALPSAAATDSGPBAGGLHAGVLEDP 60
 Db 1 MGCGGSRADAIPTPRYYESTWETESTWLTYTDSDALPSAAATDSGPBAGGLHAGVLEDP 60
 QY 61 SSNGVLRPAPGGIANPEKKONGTQCPNSOSLSSGRLTOKONGLWTEAKRDAKMSAR 120
 Db 61 SSNGVLRPAPGGIANPEKKONGTQCPNSOSLSSGRLTOKONGLWTEAKRDAKMSAR 120
 QY 121 EVAISVTEINRQMDSKRVTICIN 145
 Db 121 EVAISVTEINRQMDSKRVTICIN 145

RESULT 2

ADO48479 Standard; protein: 145 AA.

AC ADO48479;

DT 12-AUG-2004 (first entry)

XX Mouse PTH responsive gene protein.

XX PTH responsive gene; PAIGB; bone-forming; bone; bone density modulation;

XX transgenic animal; osteopathic; gene therapy; osteoporosis; mouse; murine.

OS mb sp.

XX WO2004044152-A2.

PD 27-MAY-2004.

XX 10-NOV-2003; 2003WO-US035655.

XX 12-NOV-2002; 2002US-0425532P.

PA (AMHR) WYETH.

PT Robinson JA, Stojanovic-Sabulic V, Babij P, Murrills RJ;

XX

DR WPI; 2004-420239/39.
 DR N-PSDB; ADO48478.

XX PT New nucleic acid fragment encoding a PAIGB polypeptide, useful in

PT preparing a composition for diagnosing, treating or preventing bone
 PT related disorders, e.g., osteoporosis.

PT Claim 9; SEQ ID NO 8; 169pp; English.

XX The invention relates to a novel PTH responsive gene (PAIGB) fragment

CC encoding a polypeptide. The invention further comprises: a chimeric

CC construct comprising the isolated nucleic acid fragment operatively

CC linked to suitable regulatory sequences; a host cell transformed with the

CC chimeric construct; a vector comprising the nucleic acid fragment;

CC a method for obtaining a nucleic acid fragment encoding the polypeptide; a method for

CC obtaining a polypeptide; detecting the presence of the nucleic acid

CC fragment; an antibody that specifically binds to one or more epitopes of

CC a PAIGB polypeptide; a composition for regulating bone-forming activity

CC in a mammal comprising the nucleic acid fragment, polypeptide or antibody

CC ; an agent that alter the expression of PAIGB gene or polypeptide;

CC determining whether an agent alters the expression of PAIGB mRNA;

CC screening agents for effectiveness in altering expression of the nucleic

CC acid fragment; screening for agents useful for treating bone related

CC disorders; evaluating the efficacy of treatment of a subject with a bone

CC related agent; a transgenic animal comprising the DNA; an animal model

CC for the study of bone density modulation comprising a first group of control

CC animals; studying bone mass determinant; studying the modulation of bone

CC mass; studying an effect of PAIGB on bone disorders; identifying an agent which

CC has bone forming activity; and a stably transfected cell line comprising

CC two constructs, the first construct comprising a ligand binding domain

CC linked to a DNA binding domain which is linked to an activation domain

CC all of which expression is driven by a constitutive promoter, the second

CC construct comprising multiple copies of DNA binding elements linked to a

CC minimal promoter which is linked to PAIGB cDNA, where upon the addition

CC of chemical inducer, transcription of PAIGB gene is induced. The PAIGB

CC polynucleotide has osteopathic activity. The PTH responsive gene may be

CC used to treat disorders by gene therapy. The nucleic acid is useful in

CC preparing a composition for diagnosing, treating or preventing bone

CC related disorders, e.g., osteoporosis. This sequence represents a PTH

CC responsive gene protein of the invention.

SQ Sequence 145 AA;

Query Match 97.3%; Score 746; DB 8; Length 145;

Best Local Similarity 97.2%; Pred. No. 1e-73; Mismatches 2; Indels 0; Gaps 0;

Matches 141; Conservative 2; MisMatches 2; Indels 0; Gaps 0;

QY 1 MGCGGSRADAIPTPRYYESTWETESTWLTYTDSDALPSAAATDSGPBAGGLHAGVLEDP 60
 Db 1 MGCGGSRADAIPTPRYYESTWETESTWLTYTDSDALPSAAATDSGPBAGGLHAGVLEDP 60
 QY 61 SSNGVLRPAPGGIANPEKKONGTQCPNSOSLSSGRLTOKONGLWTEAKRDAKMSAR 120
 Db 61 SSNGVLRPAPGGIANPEKKONGTQCPNSOSLSSGRLTOKONGLWTEAKRDAKMSAR 120
 QY 121 EVAISVTEINRQMDSKRVTICIN 145
 Db 121 EVAISVTEINRQMDSKRVTICIN 145

RESULT 3

AAB95018 Standard; protein: 145 AA.

AC AAB95018;

DT 26-JUN-2001 (first entry)

DB Human protein sequence SEQ ID NO:16726.

XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.
 KW XX
 OS XX Homo sapiens.
 PN XX EP1074617-A2.
 XX PD 07-FEB-2001.
 XX PP 28-JUL-2000; 2000EP-00116126.
 XX PR 29-JUL-1999; 99EP-00248036.
 PR 27-AUG-1999; 99EP-00300253.
 PR 11-JAN-2000; 2000EP-0018776.
 PR 02-MAY-2000; 2000EP-00183767.
 PR 09-JUN-2000; 2000EP-00241899.
 XX PA (HELI-) HELIX RES INST.
 XX PI Oba T, Isouai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PT Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX DR WPI; 2001-318749/34.

PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length PT cDNAs.

XX PA (HELI-) HELIX RES INST.

PS Claim 8; SEQ ID NO 16726; 2537pp + Sequence Listing; English.

CC The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises:
 CC (a) an oligo-dT primer and an oligonucleotide complementary to the
 CC complementary strand of a polynucleotide which comprises one of the 5602
 CC nucleotide sequences defined in the specification, where the full-length
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence is selected from those defined in the
 CC specification. The primer sets can be used in antisense therapy and in
 CC gene therapy. The primers are useful for synthesising polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AHH1363 to AHH13628 and
 CC AHH1363 to AHH16742 represent human cDNA sequences; AAB9245 to AAB9593
 CC represent human amino acid sequences; and AAB13629 to AAB13632 represent
 CC oligonucleotides, all of which are used in the exemplification of the
 XX present invention.

SQ Sequence 145 AA;

Query Match 84.1%; Score 645; DB 4; Length 145;
 Best Local Similarity 83.4%; Pred. No. 1.4e-62;
 Matches 121; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

Oy 1 MCGGGSRADATEPRTYYESWTRTESTWLTYTDALPSAATDSGPEAGGLHAGVLEDGP 60
 Db 1 MCGGGSRADATEPRTYYESWTRTESTWLTYTDALPSAATDSGPEAGGLHAGVLEDGL 60

Oy 61 SNGVLPAPGQIANPKKMGTCGNCNSLSSGPPKTOKNLWTEAKDAKMSAR 120
 61 PSNGVPRSTAPGGIPKPKRKTNCBQCPNPQSLSSGPPKTOKNLWTEAKDAKMSAR 120

Oy 121 EVAISVTENIKOMDRSKRVTNCIN 145
 Db 121 EVTINVIDSIQMDRSKRTKNCIN 145

Oy 121 EVAISVTENIKOMDRSKRVTNCIN 145
 Db 121 EVTINVIDSIQMDRSKRTKNCIN 145

RESULT 4
 AAO19498
 ID AAO19498 standard; protein; 145 AA.
 XX AC AAO19498;
 XX DT 20-DEC-2002 (first entry)
 XX DE HS1 protein variant.
 XX HS1 protein variant.
 XX HS1; variant; cancer; tumour; unigene cluster; cytostatic; metastasis;
 KW EST; expressed Sequence tag; colon cancer; stomach cancer; breast cancer;
 KW HS16935; HS127144; HS2; HS132793; HS3.
 XX Unidentified.
 XX OS Unidentified.
 PN DB10103694.A1.
 XX DR 01-AUG-2002.
 XX PR 26-JAN-2001; 2001DE-01003694.
 XX PR 26-JAN-2001; 2001DE-01003694.
 XX PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
 PT Brett D, Kemmer W;
 XX DR WPI; 2002-644835/70.
 N-PSDB; AAL50100.

XX PT Diagnosis and therapy of tumors, by determining expression rates of specific expressed sequence tags of the unigene cluster, and subsequently blocking their expression.

XX PS Claim 10; Page 5; 10pp; German.

The present invention relates to the use of expressed sequence tags (ESTs), or variants, of the unique cluster HS16935 (HS1), HS127144 (HS2), and/or HS132793 (HS3) for diagnosis and therapy of tumors, in which their expression rates in tumor cells and/or lymph nodes are determined. The EST Sequences are useful as prognostic markers of survival of cancer patients (high levels of EST-related mRNA are associated with a poor prognosis, specifically correlated with development of metastases); and for diagnosis and/or therapy of solid tumours, particularly of colon, stomach and breast. The present sequence is a variant of the HS1 protein shown in the exemplification of the invention.

XX SQ Sequence 145 AA;

Query Match 84.1%; Score 645; DB 5; Length 145;
 Best Local Similarity 83.4%; Pred. No. 1.4e-62;
 Matches 121; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

Oy 1 MCGGGSRADATEPRTYYESWTRTESTWLTYTDALPSAATDSGPEAGGLHAGVLEDGP 60
 Db 1 MCGGGSRADATEPRTYYESWTRTESTWLTYTDALPSAATDSGPEAGGLHAGVLEDGL 60

Oy 61 SNGVLPAPGQIANPKKMGTCGNCNSLSSGPPKTOKNLWTEAKDAKMSAR 120
 61 PSNGVPRSTAPGGIPKPKRKTNCBQCPNPQSLSSGPPKTOKNLWTEAKDAKMSAR 120

Oy 121 EVAISVTENIKOMDRSKRVTNCIN 145
 Db 121 EVTINVIDSIQMDRSKRTKNCIN 145

RESULT 5
 ABR5846
 ID ABR58646 standard; protein; 145 AA.
 XX AC ABR58646;

XX	DB	121	EVTVINVDSIQMDRSRRITKNCVN 145
XX	RESULT	6	
KW	ADC31800		
KW	ID	ADC31800 standard; protein; 145 AA.	
XX	AC	ADC31800;	
XX	DT	18-DEC-2003 (first entry)	
XX	DE	Human novel polypeptide sequence, SEQ ID NO:1882.	
XX	KW	Human; diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's disease; neurodegenerative diseases; anaemia; platelet disorder; wound; burns; ulcers; osteoporosis; autoimmune disease; cancer; molecular weight marker; food supplement; antiparkinsonian; nootropic; neuroprotective; antihaemetic; anticoagulant; thrombolytic; vulnerary; antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic; gene therapy; chromosome 8.	
XX	OS	Homo sapiens.	
XX	PN	WO2003029271-A2.	
XX	PP	17-SEP-2002; 2002WO-US0229560.	
XX	PR	17-SEP-2001; 2001US-0323469P.	
PR	20-SEP-2001; 2001US-0323887P.		
PR	13-NOV-2001; 2001US-0350666P.		
PR	08-FEB-2002; 2002US-0355145P.		
PR	08-FEB-2002; 2002US-0355257P.		
PR	12-APR-2002; 2002US-0372246P.		
PA	(E08-)	EOS BIOTECHNOLOGY INC.	
XX	PT	Afar D', Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KB;	
XX	PI	Zlotnik A;	
XX	WPI;	2003-354600/33.	
DR	N-PSDB;	ACCT2796.	
XX	PT	New genes that are up-regulated or down-regulated in cancers, useful as markers for diagnosing e.g. cancer, ischemia or heart disease, or as therapeutic targets for screening drugs for treating these diseases.	
XX	PT	Claim 12; Page 753; 76pp; English.	
CC	CC	The present invention describes an isolated nucleic acid molecule, which comprises the sequence of any of the genes that are up-regulated or down-regulated in specific cancers (e.g. about 1031 genes up-regulated in acute lymphocytic leukaemia). ACC72641 to ACC72860 represent cancer related gene nucleotide sequences which encode the proteins given in ABR58521 to ABR58709. Also described: (1) determining the presence or absence of a pathological cell in a patient; (2) an expression vector comprising a nucleic acid molecule described above; (3) a host cell comprising the vector; (4) an isolated polypeptide, which is encoded by the nucleic acid; (5) an antibody that specifically binds the polypeptide of (4); (6) specifically targeting a compound to a pathological cell in a patient by administering to the patient the antibody above; and (7) a drug screening assay. The nucleic acid is useful as diagnostic markers or therapeutic targets. In particular, the nucleic acid is useful for diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow, bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary, pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases, atherosclerosis and endometriosis. The nucleic acid is also useful in drug screening, particularly for identifying agents for treating these pathologies	
CC	CC	Sequence 145 AA:	
Query	Match	84.1%; Score 645; DB 6; Length 145;	
Best	Local Similarity	83.4%; Pred. No. 1.4e-62;	
Matches	121;	Mismatches 10; Conservative 10; Mismatches 14; Indels 0; Gaps 0;	
OY	1	MGCGGSRADAAIERYRYYESRTRETESTTWLTYTDSALPSAATSGPSEAGGLHAGVLEDP 60	
Db	1	MGGGGSRADAAIERYRYESTRETESTTWLTYTDSALPSAATSGPSEAGGLHAGVLEDP 60	
OY	61	SSNGVLRPAAPGQIANPENKQKQTCQPNQSLSGGPLTKQKQNLWTEAKRDARKMSAR 120	
Db	61	PSNGVPRSTAPGGINPEKKTCTQCPNQFQSLGGPLTKQKQNLWTEAKRDARKMPAK 120	
OY	121	EVALSVTENIRQMDRSRKRVKNCIN 145	

CC cancer. The nucleic acids may also be used as hybridisation probes or
 CC primers, and in the recombinant production of a protein. The polypeptides
 CC are also useful in generating antibodies, as molecular weight markers,
 CC and as food supplements. The present sequence represents a specifically
 CC claimed human polypeptide sequence of the invention. Note: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format directly from WIPO at
 CC ftp://ipo.int/pub/published_pct_sequences.

XX SQ Sequence 145 AA;

Query Match 84.1%; Score 645; DB 7; Length 145;
 Best Local Similarity 83.4%; Pred. No. 1.4e-62;
 Matches 121; Conservative 10; Mismatches 14; Indels 0; Gaps 0;
 QY 1 MGCGGSRADAIERPYYESWRTRETESTWLTYTDSALPSAATDGPAGGLHAGVLEDP 60
 Db 1 MGCGGSRADAIERPYYESWRTRETESTWLTYTDSALPSAATDGPAGGLHAGVLEDP 60
 QY 61 SSQVLRPAPGGIANPEKQNCQGCPQSIOSLSSGPIQKONGLWTTEAKRDAKRMSAR 120
 Db 61 SSQVLRPAPGGIANPEKQNCQGCPQSIOSLSSGPIQKONGLWTTEAKRDAKRMSAR 120
 QY 61 PSNGVPRSTAPGGIPNPKKTCETOCNPQSISSGPIQKONGLWTTEAKRDAKRMPAK 120
 Db 121 EVASVTENIRONDRSKETVKNCIN 145
 121 EVTINVNTSIOQMDRSRRTKNCIN 145

RESULT 7
 ID ADM46959
 XX standard; protein; 145 AA.

AC ADM46959;
 XX
 DT 03-JUN-2004 (first entry)

DB Brain and Acute Leukemia, Cytoplasmic alternate protein #1.
 XX acute myelogenous leukemia; gene expression; BAALC;
 KW chronic myelogenous leukemia; prostate cancer; Brain and Acute Leukemia;
 KW Cytoplasmic; exon.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 41
 /note= "encoded by GCS"
 XX
 PN WO2003040347-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 12-NOV-2002; 2002WO-US036375.
 XX
 PR 09-NOV-2001; 2001US-0348210P.
 XX
 PA (OHIS) UNIV OHIO STATE RES FOUND.
 XX
 PT Tanner SM, De La Chapell A;
 XX
 DR WPI; 2003-441564/41.
 DR N-PSDB; ADM46951.

XX PT Characterizing acute or chronic myelogenous leukemia, or prostate cancer
 PT in a patient comprises assaying for the overexpression of one or more
 PT BAALC transcripts in cells obtained from the patient.
 Disclosure; SEQ ID NO 17; 78pp; English.
 PS The invention relates to a method of characterizing acute myelogenous
 CC The invention relates to a method of characterizing acute myelogenous
 CC leukemia (AML) in a patient by assaying for the overexpression of one or
 CC more BAALC transcripts in cells obtained from the patient, where an
 CC overexpression indicates that the patient has an aggressive form of AML.

CC The methods, kits and probes are useful for characterizing acute or
 CC chronic myelogenous leukemia, or prostate cancer. They are also useful
 CC for detecting BAALC overexpression. This sequence corresponds to a BAALC
 CC (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative
 CC spliced RNA consisting of exons 1, 6 and 8.

XX SQ Sequence 145 AA;

Query Match 84.1%; Score 645; DB 7; Length 145;
 Best Local Similarity 83.4%; Pred. No. 1.4e-62;
 Matches 121; Conservative 10; Mismatches 14; Indels 0; Gaps 0;
 QY 1 MGCGGSRADAIERPYYESWRTRETESTWLTYTDSALPSAATDGPAGGLHAGVLEDP 60
 Db 1 MGCGGSRADAIERPYYESWRTRETESTWLTYTDSALPSAATDGPAGGLHAGVLEDP 60
 QY 61 SSQVLRPAPGGIANPEKQNCQGCPQSIOSLSSGPIQKONGLWTTEAKRDAKRMSAR 120
 Db 61 SSQVLRPAPGGIANPEKQNCQGCPQSIOSLSSGPIQKONGLWTTEAKRDAKRMSAR 120
 QY 121 EVASVTENIRONDRSKETVKNCIN 145
 Db 121 EVTINVNTSIOQMDRSRRTKNCIN 145

RESULT 8

ID ADO48475
 XX standard; protein; 145 AA.

AC ADO48475;
 XX
 DT 12-AUG-2004 (first entry)

DE Human PTH responsive gene protein.
 XX PTH responsive Gene; PAIGB; bone-forming; bone; bone density modulation;
 KW transgenic animal; osteopathic; gene therapy; osteoporosis; human.
 OS Homo sapiens.
 XX PN WO2004044152-A2.
 XX
 PD 27-MAY-2004.
 XX
 PF 10-NOV-2003; 2003WO-US035655.
 XX
 PR 12-NOV-2002; 2002US-0425532P.
 XX
 PA (AMHP) WYETH.
 XX
 PI Robinson JA, Stojanovic-Susulic V, Babij P, Murrills RJ;
 XX DR WPI; 2004-420299/39.
 DR N-PSDB; ADO48474.

XX PT New nucleic acid fragment encoding a PAIGB polypeptide, useful in
 PT preparing a composition for diagnosing, treating or preventing bone
 PT related disorders, e.g., osteoporosis.

XX
 PS Claim 9; SEQ ID NO 4; 169p; English.

XX The invention relates to a novel PTH responsive gene (PAIGB) fragment
 CC encoding a polypeptide. The invention further comprises: a chimeric
 CC construct comprising the isolated nucleic acid fragment operatively
 CC linked to suitable regulatory sequences; a host cell transformed with the
 CC chimeric construct; a vector comprising the nucleic acid fragment;
 CC obtaining a nucleic acid fragment encoding the polypeptide; a method for
 CC obtaining a polypeptide; detecting the presence of the nucleic acid
 CC fragment; an antibody that specifically binds to one or more epitopes of
 CC a PAIGB polypeptide; a composition for regulating bone-forming activity
 CC in a mammal comprising the nucleic acid fragment, polypeptide or antibody
 CC ; an agent that alters the expression of PAIGB gene or polypeptide;
 CC determining whether an agent alters the expression of PAIGB mRNA;

CC screening agents for effectiveness in altering expression of the nucleic acid fragment; screening for agents useful for treating bone related disorders; evaluating the efficacy of a treatment of a bone related disorder in a subject; identifying polyrepides capable of binding to PAIGB; monitoring the effectiveness of treatment of a subject with a bone related agent; a transgenic animal comprising the DNA; an animal model for the study of bone density modulation comprising a first group of animals composed of the transgenic animal and a second group of control animals; studying bone mass determinants; studying the modulation of bone mass; studying an effect of PAIGB on bone disorders; identifying an agent for treating bone related disorders; identifying whether an agent which has bone forming activity; and a stably transfected cell line comprising two constructs, the first construct comprising a ligand binding domain linked to a DNA binding domain which is linked to an activation domain all of which expression is driven by a constitutive promoter, the second construct comprising multiple copies of DNA binding elements linked to a minimal promoter which is linked to PAIGB cDNA, where upon the addition of chemical inducer, transcription of PAIGB gene is induced. The PAIGB polynucleotide has osteoplastic activity. The PTH responsive gene may be used to treat disorders by gene therapy. The nucleic acid is useful in preparing a composition for diagnosing, treating or preventing bone related disorders, e.g., osteoporosis. This sequence represents a PTH responsive gene protein of the invention.

XX Sequence 145 AA;

SQ

Query Match Best Local Similarity 84.1%; Score 645; DB 8; Length 145;
Matches 121; Conservative 10; Mismatches 14; Indels 0; Gaps 0;
Qy 1 MGCGGSRADAEPRYYESWTRTESTWLYTDSDALPSAATSGPENAGGLRAGVLDGP 60
1 MGCGGSRADAEPRYYESWTRTESTWLYTDSDALPSAATSGPENAGGLRAGVLDGP 60
Db 61 SNCVLRPAAPGIANPEKKNGCTQCPQSLSLSSGPIQKONGLWTEAKRAKRSAR 120
61 PSNCVPRSTAPGGIPNPKKCTCOPCNPQSLSSGPIQKONGLQTEAKRAKRMPC 120
Qy 121 EVAISVTENIQMDRSKRVTNIN 145
121 EVAISVTENIQMDRSKRVTNIN 145
Db 121 EVAISVTENIQMDRSKRVTNIN 145

PI Tanner SM, De La Chapell A;
XX WPT; 2003-441564/41.
DR N-PSDB; ADM46953.
XX PT Characterizing acute or chronic myelogenous Leukemia, or prostate cancer in a patient comprises assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient.
PT BAALC transcripts in cells obtained from the patient.
XX Disclosure; SEQ ID NO 19; 78pp; English.
The invention relates to a method of characterizing acute myelogenous Leukemia (AML) in a patient by assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient, where an overexpression indicates that the patient has an aggressive form of AML. The methods, kits and probes are useful for characterizing acute or chronic myelogenous leukemia, or prostate cancer. They are also useful for detecting BAALC overexpression. This sequence corresponds to a BAALC (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative spliced RNA consisting of exons 1, 6 and 8.
XX Sequence 180 AA;
SQ Query Match Best Local Similarity 80.5%; Score 617.5; DB 7; Length 180;
Matches 121; Conservative 67.2%; 10; Mismatches 14; Indels 35; Gaps 1;
Qy 1 MGCGGSRADAEPRYYESWTRTESTWLYTDSDALPSAATSGPENAGGLRAGVLDGP 60
1 MGCGGSRADAEPRYYESWTRTESTWLYTDSDALPSAATSGPENAGGLRAGVLDGP 60
Db 54 -----GVLEDGPSSNGVURPAAGCIGANPEKKNGCT 85
54 -----GVLEDGPSSNGVURPAAGCIGANPEKKNGCT 85
Db 61 KIKAPRTSVSDEGLFSASKMPLAVFSGHGMLEDGLPSNGVPRSTAPGGIPNPKKCTC 120
61 KIKAPRTSVSDEGLFSASKMPLAVFSGHGMLEDGLPSNGVPRSTAPGGIPNPKKCTC 120
Qy 86 QPNQSLSLSSGPIQKONGLWTEAKRAKRSARVEAISVTENIQMDRSKRVTNIN 145
86 QPNQSLSLSSGPIQKONGLWTEAKRAKRSARVEAISVTENIQMDRSKRVTNIN 145
Db 121 QCPNQSLSLSSGPIQKONGLQTEAKRAKRMPCVTVNVDIQQMDRSRKRVTNIN 180
121 QCPNQSLSLSSGPIQKONGLQTEAKRAKRMPCVTVNVDIQQMDRSRKRVTNIN 180

RESULT 9
ADM46951
ID ADM46961 standard; protein; 180 AA.
XX AC ADM46961;
AC ADM46961;
DT 03-JUN-2004 (first entry)
DE Brain and Acute Leukemia, Cytoplasmic alternate protein #3.
XX KW acute myelogenous leukemia; gene expression; BAALC;
KW chronic myelogenous leukemia; prostate cancer; Brain and Acute Leukemia;
KW Cytoplasmic; exon.
OS Homo sapiens.
XX Key Location/Qualifiers
FT Misc-difference 41 /note= "encoded by GCS"
FT Misc-difference 41 /note= "encoded by GCS"
XX PN WO2003040347-A2.
XX PD 15-MAY-2003.
XX PR 12-NOV-2002; 2002WO-US036375.
XX PR 09-NOV-2001; 2001US-0348210P.
XX PA (OHIS) UNIV OHIO STATE RES FOUND.
XX DR WPI; 2003-441564/41.

DR N-PSDB; ADO46955.

XX PT Characterizing acute or chronic myelogenous leukemia, or prostate cancer
 PT in a patient comprises assaying for the overexpression of one or more
 PT BIALC transcripts in cells obtained from the patient.
 XX
 PS Disclosure; SEQ ID NO 21; 78pp; English.

The invention relates to a method of characterizing acute myelogenous
 leukemia (AML) in a patient by assaying for the overexpression of one or
 more BIALC transcripts in cells obtained from the patient, where an
 overexpression indicates that the patient has an aggressive form of AML.
 The methods, kits and probes are useful for characterizing acute or
 chronic myelogenous leukemia, or prostate cancer. They are also useful
 for detecting BIALC overexpression. This sequence corresponds to a BIALC
 (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative
 spliced RNA consisting of exons 1, 6 and 8.
 XX
 SQ Sequence 149 AA;

Query Match 61.7%; Score 473.5; DB 7; Length 149;
 Best Local Similarity 66.0%; Pred. No. 1.2e-43; Matches 95; Conservative 2; Mismatches 12; Indels 35; Gaps 1;

QY 1 MGCGGSRADATEPRYYESWTRTESTWLTYTDSDALPSAATDSGPEAGGLHA-----
 Db 1 MGCGGSRADATEPRYYESWTRTESTWLTYTDSDALPSAATDSGPEAGGLHSVLEAKS 60
 QY 54 -----GVEDGGSSNGYTPAAMPGGTANPEKCONCCT 85
 Db 61 KIKAPAPTDVSDEGLPSASKMAPLAVFSGHGMEDGLPNSNGYPRSTAGGIPNPERKNCET 120
 QY 86 QCPNQSLSGGPLTKONGJMTT 109
 Db 121 QCPNFSLSGGPLTKONGJQTT 144

RESULT 11
 ADQ81902
 ID ADO81902 Standard; protein; 92 AA.
 XX
 AC ADQ81902;
 XX
 DT 09-SEP-2004 (first entry)
 DE Human dioxygenase 10.12.
 XX
 KW Human; enzyme; dioxygenase 10.12; malignant tumour; inflammation;
 KW immunological disease; haemopathy; HIV infection.
 OS Homo sapiens.
 XX
 PN CN1347478-A.
 XX
 PD 17-APR-2002.
 XX
 PP 29-SEP-2000; 2000CN-00125495.
 PR 29-SEP-2000; 2000CN-00125495.
 XX
 PA (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.
 XX
 PT Mao Y, Xie Y;
 XX
 DR WPI; 2002-502506/55.
 DR N-PSDB; ADQ81901.

XX New polypeptide human dioxygenase 10.12 and polynucleotides encoding this
 PT polypeptide, useful for treating various diseases, such as malignant
 PT tumors, inflammation, immunological diseases, hemopathy and HIV
 PT infection.
 XX
 PS Claim 1; SEQ ID NO 2; 33pp; Chinese.

XX The present invention discloses a new kind of polypeptide, human

CC dioxygenase 10.12, polynucleotides encoding this polypeptide, a DNA
 CC recombination process to produce the polypeptide and antagonist against
 CC the polypeptide. The present invention also disclose the method of
 CC applying the polypeptide in treating various diseases, such as malignant
 CC tumours, inflammations, immunological diseases, haemopathy and HIV
 CC infection. The present sequence is the human dioxygenase 10.12.

XX SQ Sequence 92 AA;
 Query Match 43.7%; Score 335.5; DB 5; Length 92;
 Best Local Similarity 72.7%; Pred. No. 1.1e-28; Matches 64; Conservative 9; Mismatches 10; Indels 5; Gaps 1;
 QY 58 DGPSNGVPRPAARGGIANPEKCONCCTCOPNSOSLSISPLTKONGJMTTEAKRDARM 117
 Db 10 DSPEIYN----APGGIPNPEKKKTCOTCPNPOSLISGSPLTOKONGJQTEAKRDARM 64

RESULT 12
 ADQ8481
 ID ADO8481 Standard; protein; 54 AA.
 XX
 AC ADQ8481;
 XX
 DT 12-AUG-2004 (first entry)
 DE Mouse PTH responsive gene exon 2 splice variant.
 XX
 KW PTH responsive gene; PAIGB; bone-forming; bone; bone density modulation;
 KW transgenic animal; osteopathic; gene therapy; osteoporosis; mouse;
 KW murine.
 XX
 OS Mus SP.
 XX
 PN WO2004044152-A2.
 XX
 PD 27-MAY-2004.
 XX
 PF 10-NOV-2003; 2003WO-US035655.
 XX
 PR 12-NOV-2002; 2002US-042553P.
 XX
 PA (AMMP) WYETH.
 XX
 PT Robinson JA, Stojanovic-Sabulic V, Babij P, Murrills RJ;
 XX
 DR WPI; 2004-420299/39.
 DR N-PSDB; ADQ8480.
 XX
 PT New nucleic acid fragment encoding a PAIGB polypeptide, useful in
 PT preparing a composition for diagnosing, treating or preventing bone
 PT related disorders, e.g., osteoporosis.
 XX
 PS Claim 9; SEQ ID NO 10; 169pp; English.

XX The invention relates to a novel PTH responsive gene (PAIGB) fragment
 CC encoding a polypeptide. The invention further comprises: a chimeric
 CC construct comprising the isolated nucleic acid fragment operatively
 CC linked to suitable regulatory sequences; a host cell transformed with the
 CC chimeric construct; a vector comprising the nucleic acid fragment,
 CC obtaining a nucleic acid fragment encoding the polypeptide; a method for
 CC obtaining a polypeptide; detecting the presence of the nucleic acid
 CC fragment; an antibody that specifically binds to one or more epitopes of
 CC a PAIGB polypeptide; a composition for regulating bone-forming activity
 CC in a mammal comprising the nucleic acid fragment, polypeptide or antibody
 CC ; an agent that alters the expression of PAIGB gene or polypeptide mRNA;
 CC determining whether an agent alters the expression of PAIGB mRNA;

CC screening agents for effectiveness in altering expression of the nucleic acid fragment; screening for agents useful for treating bone related disorders; evaluating the efficacy of a treatment of a bone related disorder in a subject; identifying polypeptides capable of binding to PAIGB; monitoring the effectiveness of treatment of a subject with a bone related agent; a transgenic animal comprising the DNA; an animal model for the study of bone density modulation comprising a first group of animals composed of the transgenic animal and a second group of control animals; studying bone mass determinants; studying the modulation of bone mass; studying an effect of PAIGB on bone disorders; identifying an agent for treating bone related disorders; identifying whether an agent which has bone forming activity; and a stably transfected cell line comprising two constructs, the first construct comprising a ligand binding domain linked to a DNA binding domain which is linked to an activation domain all of which expression is driven by a constitutive promoter, the second construct comprising multiple copies of a DNA binding elements linked to a minimal promoter which is linked to PAIGB cDNA, where upon the addition of chemical inducer, transcription of PAIGB gene is induced. The PAIGB polypeptide has osteoplastic activity. The PTH responsive gene may be used to treat disorders by gene therapy. The nucleic acid is useful in preparing a composition for diagnosing, treating or preventing bone related disorders, e.g., osteoporosis. This sequence represents a PTH responsive gene protein of the invention.

XX Sequence 54 AA;

SQ

Query Match 38.3%; Score 294; DB 8; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.9e-24;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MGCGGSRADAIERRYYESWTTETESTWLTYTDSALPSAATDSGPEAGGLHAG 54
Db 1 MGCGGSRADAIERRYYESWTTETESTWLTYTDSALPSAATDSGPEAGGLHAG 54

RESULT 13

ID ADM46952

ID ADM46952 standard; protein; 73 AA.

XX AC ADM46952;

XX DT 03-JUN-2004 (first entry)

DB Brain and Acute Leukemia, Cytoplasmic alternate protein #4.

KW acute myelogenous leukemia; gene expression; BAALC;

KW chronic myelogenous leukemia; prostate cancer; Brain and Acute Leukemia;

KW cytoplasmic; exon.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Misc-difference 41 /note= "encoded by GCS"

FT WO2003040347-A2.

XX PN

XX PD 15-MAY-2003.

XX PP 12-NOV-2002; 2002WO-US036375.

XX PR 09-NOV-2001; 2001US-0348210P.

XX PA (OHIS) UNIV OHIO STATE RES FOUND.

XX PI Tanner SM, De La Chapell A;

XX DR WPI; 2003-441564/41.

XX N-PSDB, ADM46952.

XX Disclosure: SEQ ID NO 18; 78pp; English.

XX

CC Characterizing acute or chronic myelogenous leukemia, or prostate cancer in a patient comprises assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient.

CC Disclosure: SEQ ID NO 18; 78pp; English.

CC

CC The invention relates to a method of characterizing acute myelogenous leukemia (AML) in a patient by assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient, where an overexpression indicates that the patient has an aggressive form of AML.

CC The methods, kits and probes are useful for characterizing acute or chronic myelogenous leukemia, or prostate cancer. They are also useful for detecting BAALC overexpression. This sequence corresponds to a BAALC (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative spliced RNA consisting of exons 1, 6 and 8.

XX Disclosure: SEQ ID NO 20; 78pp; English.
PS
XX The invention relates to a method of characterizing acute myelogenous leukemia (AML) in a patient by assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient, where an overexpression indicates that the patient has an aggressive form of AML. The methods, kits and probes are useful for characterizing acute or chronic myelogenous leukemia, or prostate cancer. They are also useful for detecting BAALC overexpression. This sequence corresponds to a BAALC (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative spliced RNA consisting of exons 1, 6 and 8.

XX Sequence 73 AA;
SQ

Query Match 37.5%; Score 288; DB 7; Length 73;
Best Local Similarity 91.4%; Pred. No. 1.3e-23;
Matches 53; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 MGCGGSRADAIERRYYESWTTETESTWLTYTDSALPSAATDSGPEAGGLHAGLVED 58
Db 1 MGCGGSRADAIERRYYESWTTETESTWLTYTDSALPSAATDSGPEAGGLHAGLVED 58

RESULT 14

ID ADM46960

ID ADM46960 standard; protein; 54 AA.

XX AC ADM46960;

XX DT 03-JUN-2004 (first entry)

DB Brain and Acute Leukemia, Cytoplasmic alternate protein #2.

XX KW acute myelogenous leukemia; gene expression; BAALC;

KW chronic myelogenous leukemia; prostate cancer; Brain and Acute Leukemia;

KW cytoplasmic; exon.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Misc-difference 41 /note= "encoded by GCS"

FT WO2003040347-A2.

XX PN

XX PD 15-MAY-2003.

XX PP 12-NOV-2002; 2002WO-US036375.

XX PR 09-NOV-2001; 2001US-0348210P.

XX PA (OHIS) UNIV OHIO STATE RES FOUND.

XX PI Tanner SM, De La Chapell A;

XX DR WPI; 2003-441564/41.

XX N-PSDB, ADM46952.

XX Disclosure: SEQ ID NO 18; 78pp; English.

XX

CC Characterizing acute or chronic myelogenous leukemia, or prostate cancer in a patient comprises assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient.

CC Disclosure: SEQ ID NO 18; 78pp; English.

CC

CC The invention relates to a method of characterizing acute myelogenous leukemia (AML) in a patient by assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient, where an overexpression indicates that the patient has an aggressive form of AML.

CC The methods, kits and probes are useful for characterizing acute or chronic myelogenous leukemia, or prostate cancer. They are also useful for detecting BAALC overexpression. This sequence corresponds to a BAALC (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative

CC spliced RNA consisting of exons 1, 6 and 8.
 CC
 XX Sequence 54 AA:
 SQ
 Query Match 36.2%; Score 278; DB 7; Length 54;
 CC Best Local Similarity 94.4%; Pred. No. 1.1e-22; Mismatches 2; Indels 0; Gaps 0;
 CC Matches 51; Conservative 1; Mismatches 2;
 QY 1 MGCGGSRADIAEPRYYESWRTETSTWLTTDSDALPSAATDSGPEAGGLHAG 54
 Db 1 MGCGGSRADIAEPRYYESWRTETSTWLTTDSDALPSAATDSGPEAGGLHSG 54

RESULT 15

ADD48477

ID ADD48477 standard; protein; 54 AA.

XX

AC ADD48477;

XX

DT 12-AUG-2004 (First entry)

XX

DE Human PTH responsive gene protein exon 2 splice variant.

XX

KW PTH responsive gene; PAIGB; bone-forming; bone; bone density modulation; transgenic animal; osteopathic; gene therapy; osteoporosis; human.

XX

OS Homo sapiens.

XX

PN WO200404152-A2.

XX

PD 27-MAY-2004.

XX

PP 10-NOV-2003; 2003WO-US035655.

XX

PR 12-NOV-2002; 2002US-0425532P.

XX

PA (AMHRP) WYETH.

XX

PT Robinson JA, Stojanovic-Subolic V, Babij P, Murrills RJ;

XX

DR WO; 2004-420299/39.

XX

N-PSDB; ADD48476.

XX

PT New nucleic acid fragment encoding a PAIGB polypeptide, useful in preparing a composition for diagnosing, treating or preventing bone related disorders, e.g., osteoporosis.

XX

PS Claim 9; SEQ ID NO 6; 169pp; English.

XX

CC The invention relates to a novel PTH responsive gene (PAIGB) fragment encoding a polypeptide. The invention further comprises: a chimeric construct comprising the isolated nucleic acid fragment operatively linked to suitable regulatory sequences; a host cell transformed with the chimeric construct; a vector comprising the nucleic acid fragment; obtaining a nucleic acid fragment encoding the polypeptide; a method for obtaining a polypeptide; detecting the presence of the nucleic acid fragment; an antibody that specifically binds to one or more epitopes of a PAIGB polypeptide; a composition for regulating bone-forming activity in a mammal comprising the nucleic acid fragment, polypeptide or antibody ; an agent that alters the expression of PAIGB gene or polypeptide; determining whether an agent alters the expression of PAIGB mRNA; screening agents for effectiveness in altering expression of the nucleic acid fragment; screening for agents useful for treating bone related disorders; evaluating the efficacy of a treatment of a bone related disorder in a subject; identifying polypeptides capable of binding to PAIGB; monitoring the effectiveness of treatment of a subject with a bone related agent; a transgenic animal comprising the DNA; an animal model for the study of bone density modulation comprising a first group of animals composed of the transgenic animal and a second group of control animals; studying bone mass determinants; studying the modulation of bone mass; studying an effect of PAIGB on bone disorders; identifying an agent for treating bone related disorders; identifying whether an agent which has bone forming activity; and a stably transfected cell line comprising

CC two constructs, the first construct comprising a ligand binding domain linked to a DNA binding domain which is linked to an activation domain all of which expression is driven by a constitutive promoter, the second construct comprising multiple copies of DNA binding elements linked to a minimal promoter which is linked to PAIGB cDNA, where upon the addition of chemical inducer, transcription of PAIGB gene is induced. The PAIGB polymucleotide has osteopathic activity. The PTH responsive gene may be used to treat disorders by gene therapy. The nucleic acid is useful in preparing a composition for diagnosing, treating or preventing bone related disorders, e.g., osteoporosis. This sequence represents a PTH responsive gene protein of the invention.

SQ Sequence 54 AA;

Query Match 36.2%; Score 278; DB 8; Length 54;

CC Best Local Similarity 94.4%; Pred. No. 1.1e-22; Mismatches 2; Indels 0; Gaps 0;

CC Matches 51; Conservative 1; Mismatches 2;

QY 1 MGCGGSRADIAEPRYYESWRTETSTWLTTDSDALPSAATDSGPEAGGLHAG 54

Db 1 MGCGGSRADIAEPRYYESWRTETSTWLTTDSDALPSAATDSGPEAGGLHSG 54

Search completed: May 20, 2006, 20:18:06
Job time : 86 secs

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OM protein - protein search, using SW model

Run on: May 20, 2006, 21:10:42 ; Search time 51 Seconds
{without alignments}
248.862 Million cell updates/sec

Title: Perfect score: US-10-705-716A-2

Sequence: 1 MCGGGGRADATIIRRYYESWT.....VBNIRQMDRSKRVNACIN 145

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 8753628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: /EMC_Celerra_SIDS3/podata/2/1aa/5_COMBO.pep:*
- 2: /EMC_Celerra_SIDS3/podata/2/1aa/6_COMBO.pep:*
- 3: /EMC_Celerra_SIDS3/podata/2/1aa/_COMB.pep:*
- 4: /EMC_Celerra_SIDS3/podata/2/1aa/H_COMBO.pep:*
- 5: /EMC_Celerra_SIDS3/podata/2/1aa/PCTUS_COMBO.pep:*
- 6: /EMC_Celerra_SIDS3/podata/2/1aa/RE_COMBO.pep:*
- 7: /EMC_Celerra_SIDS3/podata/2/1aa/backfilesl.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARES

Result No.	Score	Query Match Length	DB ID	Description
1	92.5	12.1	694	Sequence 7117, Application US/09949016
2	92.5	12.1	778	Patent No. 5198347
3	83.8	11.0	726	Sequence 8115, Application US-09-949-016-7117
4	83.5	10.9	700	Sequence 2, Applicant No. 5198347
5	83	10.8	1433	Sequence 60, Applicant No. 5198347
6	79.5	10.4	286	Sequence 176, Applicant No. 5198347
7	79.5	10.4	286	Sequence 176, Applicant No. 5198347
8	79.5	10.4	305	Sequence 174, Applicant No. 5198347
9	79.5	10.4	305	Sequence 174, Applicant No. 5198347
10	79.5	10.4	661	Sequence 174, Applicant No. 5198347
11	79.5	10.4	661	Sequence 174, Applicant No. 5198347
12	79.5	10.4	1013	Sequence 553, Applicant No. 5198347
13	79.5	10.4	1013	Sequence 553, Applicant No. 5198347
14	78.5	10.2	2516	Sequence 2, Applicant No. 5198347
15	78.5	10.2	2516	Sequence 2, Applicant No. 5198347
16	78.5	10.2	2516	Sequence 2, Applicant No. 5198347
17	78	10.2	724	Sequence 1, Applicant No. 5198347
18	78	10.2	885	Sequence 10, Applicant No. 5198347
19	77.5	10.1	215	Sequence 104, Applicant No. 5198347
20	77.5	10.1	445	Sequence 433, Applicant No. 5198347
21	77.5	10.1	445	Sequence 433, Applicant No. 5198347
22	77.5	10.1	445	Sequence 433, Applicant No. 5198347
23	77.5	10.1	445	Sequence 433, Applicant No. 5198347
24	77.5	10.1	445	Sequence 433, Applicant No. 5198347
25	77.5	10.1	445	Sequence 433, Applicant No. 5198347
26	77.5	10.1	445	Sequence 433, Applicant No. 5198347

RESULT 1

SEQ ID NO: 7117
SEQUENCE LENGTH: 694
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-7117

Query Match Score: 92.5; DB 2; Length: 694;
Best Local Similarity: 31.9%; Pred. No. 0 12; Gaps: 3;
Matches: 30; Conservative: 7; Mismatches: 32; Indels: 25; Gaps: 3;

QY	Db	31 TDSDALPAAATSGPENGLH-----AGVNRDGPSSNGTIRPAAP--
QY	Db	233 TDSEVSOSPAKNSKPKVNSQHQSAPAVPTPSGPPPAASALTTPRNGVAPAAPPS
QY	Db	293 ALGPKASPAKSNSGTPAPIQKVAPPAPSGF

RESULT 2

5198347-4

; PATENT NO. 5198347
; APPLICANT: Miller, Louis H.; Adams, John H.; Kaslow,
; DAVIC C.; FANG, XIANGDOU
; TITLE OF INVENTION: DNA ENCODING PLASMODIUM VIVAX AND
; PLASMODIUM KNOWLES DUFFY RECEPTOR
; NUMBER OF SEQUENCES: 27
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/554,837
; FILING DATE: 20-JUL-1990

ALIGNMENTS

;SEQ ID NO:4:
; LENGTH: 778
; 5198347-4

Query Match
Best Local Similarity 12.1%; Score 92.5; DB 7; Length 778;
Matches 29; Conservative 33; Predicted No. 0.14; Mismatches 44; Indels 3; Gaps 3;

QY 31 TDSDALPSAATNDSGPPEAGGHAGVLEDPGSSNGV-LRPAAPGGTANPERKKNC-GTQP 88
Db 352 TYSVSPVSPVGKDSGPSTSAHALAGENGWVHNGDTEPKEDGKADPOXDKIEVKGKDT 411

QY 89 NSQSLSS-GRLTQKONGLWTTEAKRDAK 115
Db 412 DDRSOGSGLGPHTDERATLGTHMEKDTE 439

RESULT 3
US-09-328-352-8115
Sequence 8115, Application US/09328352
Patent No. 6562558

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTG39-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 8115
LENGTH: 726
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-8115

Query Match
Best Local Similarity 11.0%; Score 84; DB 2; Length 726;
Matches 27; Conservative 8; Mismatches 22; Indels 20; Gaps 4;

QY 2 GCGGSSRADATEPRYYESWTTTESTWLTYTDSDALPSA--ATATSG----PEAGGLHAG 54
Db 181 GPGAGREDWVEPDNIVNGDEKE--WLAKRNISEALAGSNIAIENGLIVNP----- 231

QY 55 VLRDOPSSNGVLRPAP 71
Db 232 ---GPOASGDPRSAAP 244

RESULT 4
US-09-408-647A-2
Sequence 2, Application US/09408647A
Patent No. 6399888

GENERAL INFORMATION:
APPLICANT: Kobayashi, Donald
TITLE OF INVENTION: Chitinase Gene from Stenotrophomonas
FILE REFERENCE: RUT-Cook 98-0090
CURRENT APPLICATION NUMBER: US/09/408,647A

CURRENT FILING DATE: 1999-08-26
PRIOR APPLICATION NUMBER: 60/098,036
PRIOR FILING DATE: 1998-08-27
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 700
TYPE: PRT
ORGANISM: Stenotrophomonas maltophilia

FEATURE: NAME/KEY: SIGNAL
LOCATION: (1)..(41)
NAME/KEY: DOMAIN
LOCATION: (196)..(290)
NAME/KEY: DOMAIN

RESULT 5
US-09-407-558B-60
Sequence 60, Application US/09407558B
Patent No. 6943556

GENERAL INFORMATION:
APPLICANT: Bubby, Robert
APPLICANT: Call, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
APPLICANT: Maxon, Mary
APPLICANT: Milne, Todd
APPLICANT: No. 694356an, Thea
APPLICANT: Royer, John
APPLICANT: Salama, Sofie
APPLICANT: Sherman, Amir
APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 10272-130
CURRENT APPLICATION NUMBER: US/09/487,558B
CURRENT FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/487,558
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 446

NUMBER OF SEQ ID NOS: 446
SEQ ID NO 60
LENGTH: 1433
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-09-407-558B-60

Query Match
Best Local Similarity 10.8%; Score 83; DB 2; Length 1433;
Matches 32; Conservative 15; Mismatches 50; Indels 12; Gaps 4;

QY 36 LPSAAATSGPPEAGGHAGVLEDPGSSNGV-LRPAAPGGTANPERKKNC-GTQP 95
Db 927 LPPATTTSKPLQSGQSNSLNRPTPNKR-----ENPEHVLGNDNSNNNSA 979

QY 96 G--PLTQKONGLWTTEAKRDAKMSARSAVAISTENIR-QMRSKRT 140
Db 980 GHSMINTNTNGNKRKVKDAKE-NAKQGIGSKGENANFQNTKOMS 1027

RESULT 6
US-09-071-035-176
Sequence 176, Application US/09071035
Patent No. 6448043

GENERAL INFORMATION:

APPLICANT: Gil H. Choi
 TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
 NUMBER OF SEQUENCES: 496
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: Maryland
 COUNTRY: USA
 ZIP: 20850

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
 COMPUTER: HP Vectra 486/33
 OPERATING SYSTEM: MSDOS version 6.2
 SOFTWARE: ASCII Text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/071,035
 FILING DATE: 29-Jul-2002
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 09/071,035
 FILING DATE: 1998-05-04
 APPLICATION NUMBER: US 60/046,655
 FILING DATE: 1997-05-16
 APPLICATION NUMBER: US 60/044,031
 FILING DATE: 1997-05-06
 APPLICATION NUMBER: US 60/065,009
 FILING DATE: 1997-11-14
 ATTORNEY/AGENT INFORMATION:
 NAME: Human, Mark J.
 REGISTRATION NUMBER: 46,789
 REFERENCE DOCKET NUMBER: PB369P1D1

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/071,035
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: A. Andis Brookes
 REGISTRATION NUMBER: 36,373
 REFERENCE DOCKET NUMBER: PB369P2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 309-8504
 TELEFAX: (301) 309-5112
 INFORMATION FOR SEQ ID NO: 176:
 IS-BQSEQUENCE CHARACTERISTICS:
 LENGTH: 286 amino acids
 TYPE: amino acid
 STRANDBNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 STRANDBNESS: Single
 TOPLOGY: Linear
 TYPE: amino acid
 LENGTH: 286 amino acids
 US-09-071-035-176

Query Match 10.4%; Score 79.5; DB 2; Length 286;

Best Local Similarity 26.6%; Pred. No. 1.1; Matches 47; Conservative 16; Mismatches 73; Indels 41; Gaps 9;

Query 3 CGG-----SRADAIPEPRYYESW---TRETESTWLTYTDALPSAAT-DSGPAG 49
 Db 1 CGGKSTENTDSRSAASTIVESTKASATKESSK-ATKSSDAKPSGTTDASKATAS 59
 Query 50 GLHAGVLDGPGSNGVIRPAAPGGIANBEKOM-CGTQCPN--SQSISSGPITQOKQNL 105
 Db 60 STKEA-----ANNSAKRSPAKNANDQANVOLNLANMFPQGILPOAIIISOTNNF 113
 Query 106 WTEBAKDKRMSARAEVAVLVIENIRQMD-RSKVT-----XKCIN 145
 Db 114 LTAAITSQADQNFRVLYYAEKEAIPVNDARVNQLTPISSFEKKTYGDAEAKNAVN 170

RESULT 7
 US-10-206-576-176
 Sequence 176, Application US/10206576
 ; Patent No. 6913907
 ; GENERAL INFORMATION:
 ; APPLICANT: Choi et al.

TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
 NUMBER OF SEQUENCES: 497
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: Maryland
 COUNTRY: USA
 ZIP: 20850

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
 COMPUTER: HP Vectra 486/33
 OPERATING SYSTEM: MSDOS version 6.2
 SOFTWARE: ASCII Text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/071,035
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:

COMPUTER READABLE FORM:
 MEDIUM TYPE: CD-R
 COMPUTER: Dell Latitude
 COMPUTER: Dell Latitude

ATTORNEY/AGENT INFORMATION:

NAME: A. Anders Brookes

REGISTRATION NUMBER: 36,373

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 174:

SEQUENCE CHARACTERISTICS:

LENGTH: 305 amino acids

TYPE: amino acid

STRANDEDNESS: Single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-071-035-174

Query Match 10.4%; Score 79.5; DB 2; Length 305;
 Best Local Similarity 26.6%; Pred. No. 1.2; Mismatches 73; Indels 41; Gaps 9;
 Matches 47; Conservative 16; MisMatches 73; Indels 41; Gaps 9;

QY 3 CGG-----SRAADEPRYESW---TREESTWLTYTDALPSAAT-DSGPENG 49

Db 20 CGGGKSTENTDRSSAAESTTVECTIKASATKESSK-ATTKSSAKPSCTTADSKATAS 78

QY 50 GLHAGVLEDGPPSSNGVLRPAPGGIANPEKKMN-CGTCOPN--SOSLSSGPIUTOKONGL 105

Db 79 STKEA-----ANNSAEKQSPAKNNANPDDQANQVNQLNAMMFPQGQGLPQALTSQTNF 132

QY 106 WTEAKRDAKMSAREVAISVTENIRQMD-RSKRT-----KNCIN 145

Db 133 LTATTSDAQNFRVLYYEKEAIPVNDARVNQLTPISSFEKRTYGSDAEAKNAVN 189

RESULT 10

US-10-076-622-552

Sequence 552, Application US/10076622

; Patent No. 6950361

; GENERAL INFORMATION:

; APPLICANT: Houghton, Raymond L.

; APPLICANT: Sleath, Paul R.

; APPLICANT: Persing, David H.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: 210121_470C11

; CURRENT APPLICATION NUMBER: US/10/076,622

; NUMBER OF SEQ ID NOS: 627

; CURRENT FILING DATE: 2002-02-13

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 552

; LENGTH: 661

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-076-622-552

Query Match 10.4%; Score 79.5; DB 2; Length 661;
 Best Local Similarity 21.5%; Pred. No. 3.6; Mismatches 58; Indels 49; Gaps 7;
 Matches 37; Conservative 28; MisMatches 58; Indels 49; Gaps 7;

QY 7 RADIAEP----RYESTWLTYTDALPSAAT-DSGPENG 60

Db 401 RADILPESKSKDYEBSWDSLCLTVSKQDVCLPKAHOKEDKIN---GKLEBSP 456

QY 61 SSGVGVRRAAPGGIANPEKKMN-CGTCOPN--SOSLSSGPIUTOKONGL 90

Db 457 DNGPLKSPCRMVKSIPTKALEMDMOTPKAEPPEKPSAFEPAIEMOKSPVNPALKELNE 516

QY 91 QSLSSG----PLTOKONGL---WTEAKRDAKMSAREVAISVTENIRQMDR 135

Db 517 QTRADOMPSKSKQKONVENSADSERET--VSQKDVCVPKATHQEMDK 566

RESULT 11

US-10-124-805-552

; Sequence 552, Application US/1012405

; General Information:

; Patent No. 6950518

; APPLICANT: Houghton, Raymond L.

; APPLICANT: Sleath, Paul R.

; APPLICANT: Persing, David H.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: 210121_470C12

; SEQUENCE CHARACTERISTICS:

; LENGTH: 305 amino acids

Query Match 10.2%; Score 78.5; DB 2; Length 2516;
 Best Local Similarity 22.4%; Pred. No. 33; Mismatches 61; Indels 53; Gaps 8;
 Matches 39; Conservative 21; Mismatches 61; Indels 53; Gaps 8;

QY 3 CGGSRADATEPRY--YESWTRTESTWLTYTDSALPSAATSGPENAGGLAHGVLEDGP 60
 Db 207 CGGGCGISAPPRLPEEAMQLOPQ----NSVTSGTNSFPSSGG----GR 249
 QY 61 SNGVLRPAPGGTANPEKEMC-----GTC-----PNS 90
 Db 250 DDNSYY--SAVGGSSSNSNCNDITGDNSTLHGLGVGVCFTADCDNSEDDDGDPN 307
 QY 91 QSLSSGPL-TQKQNLWTTEAKRDAKMSAREVAISVTENIRQMDRSKRVTKC 143
 Db 308 QDLSQTARTAIVAAVAAKEQAOEQSLADE-SFSDRRQDADEDVRIODC 360

RESULT 15

US-08-895-590-2
 ; Sequence 2, Application US/08895590
 ; Patent No. 6207410
 ; GENERAL INFORMATION:
 ; APPLICANT: Hall, Linda M.
 ; APPLICANT: Ren, Bejian
 ; APPLICANT: Zheng, Wei
 ; APPLICANT: Dubaid, Manuel Marcel Paul
 ; TITLE OF INVENTION: Genes Encoding an Insect Calcium Channel
 ; NUMBER OF SEQUENCES: 101
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BURNS, DOANE, SWCKER & MATHIS, LLP
 ; STREET: 699 Prince Street
 ; CITY: Alexandria
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22314-3187
 ; COMPUTER READABLE FORM:
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/895,590
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McCowan, Malcolm M.
 ; REGISTRATION NUMBER: 39,300
 ; REFERENCE/DOCKET NUMBER: 022650-263
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-836-6620
 ; TELEFAX: 703-836-2021
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2516 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein

US-08-895-590-2

Query Match 10.2%; Score 78.5; DB 2; Length 2516;
 Best Local Similarity 22.4%; Pred. No. 33; Mismatches 61; Indels 53; Gaps 8;
 Matches 39; Conservative 21; Mismatches 61; Indels 53; Gaps 8;

QY 3 CGGSRADATEPRY--YESWTRTESTWLTYTDSALPSAATSGPENAGGLAHGVLEDGP 60
 Db 207 CGGGCGISAPPRLPEEAMQLOPQ----NSVTSGTNSFPSSGG----GR 249
 QY 61 SNGVLRPAPGGTANPEKEMC-----GTC-----PNS 90
 Db 250 DDNSYY--SAVGGSSSNSNCNDITGDNSTLHGLGVGVCFTADCDNSEDDDGDPN 307

Search completed: May 20, 2006, 21:21:21
 Job time : 52 sec

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OM protein - protein search, using sw model

Run on: May 20, 2006, 21:21:43 ; Search time 74 Seconds

Perfect score: US-10-705-716A-2

Sequence: MGCGSRADAIPEPRYESWT.....VTEINIRQMDRSKRVTKNCIN 145

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 sqbs, 463214958 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA Main: *

1: /EMC_Celerra_S1BS3/ptodata/2/pupbaa/US07_PUBCOMB.pep:*

2: /EMC_Celerra_S1BS3/ptodata/2/pupbaa/US08_PUBCOMB.pep:*

3: /EMC_Celerra_S1BS3/ptodata/2/pupbaa/US09_PUBCOMB.pep:*

4: /EMC_Celerra_S1BS3/ptodata/2/pupbaa/US10A_PUBCOMB.pep:*

5: /EMC_Celerra_S1BS3/ptodata/2/pupbaa/US10B_PUBCOMB.pep:*

6: /EMC_Celerra_S1BS3/ptodata/2/pupbaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description	
1	747	100.0	145	4	US-10-705-716A-2	
2	97.3	145	4	US-10-705-716A-2	Sequence 2, Appli	
3	645	84.1	145	4	US-10-705-716A-2	Sequence 8, Appli
4	645	84.1	145	4	US-10-705-716A-2	Sequence 17, Appli
5	645	84.1	145	4	US-10-705-716A-2	Sequence 30, Appli
6	617.5	80.5	180	4	US-10-705-716A-2	Sequence 4, Appli
7	473.5	61.7	149	4	US-10-705-716A-2	Sequence 19, Appli
8	294	38.3	54	4	US-10-705-716A-2	Sequence 21, Appli
9	288	37.5	73	4	US-10-705-716A-2	Sequence 10, Appli
10	278	36.2	54	4	US-10-705-716A-2	Sequence 20, Appli
11	278	36.2	54	4	US-10-705-716A-2	Sequence 18, Appli
12	272	35.5	80	4	US-10-705-716A-2	Sequence 6, Appli
13	140	18.3	25	4	US-10-705-716A-2	Sequence 22, Appli
14	99	12.9	18	4	US-10-705-716A-2	Sequence 37, Appli
15	94	12.3	147	4	US-10-705-716A-2	Sequence 35, Appli
16	93	12.1	394	4	US-10-705-716A-2	Sequence 40905, A
17	89	11.6	16	4	US-10-705-716A-2	Sequence 236244, A
18	87.5	11.4	260	5	US-10-705-716A-2	Sequence 40258, A
19	87.5	11.4	592	5	US-10-705-716A-2	Sequence 45966, A
20	85.5	11.1	264	4	US-10-705-716A-2	Sequence 275422, A
21	85.5	11.1	274	4	US-10-705-716A-2	Sequence 55588, A
22	85	11.1	450	4	US-10-705-716A-2	Sequence 137075, A
23	84	11.1	718	4	US-10-705-716A-2	Sequence 45268, A
24	83	10.8	1433	3	US-10-705-716A-2	Sequence 60, Appli
25	83	10.8	1433	4	US-10-705-716A-2	Sequence 112, Appli
26	82.5	10.8	514	6	US-10-705-716A-2	Sequence 18211, A
27	82.5	10.8	539	4	US-10-705-716A-2	Sequence 227399, A

ALIGNMENTS

RESULT 1
US-10-705-716A-2

; Sequence 2, Application US/10705-716A

; Publication No. US20040146906A1

; GENERAL INFORMATION:

; APPLICANT: Stojanovic-Subolic, Vedrana

; APPLICANT: Babij, Philip

; APPLICANT: Murrills, Richard John

; FILE REFERENCE: AML0401

; CURRENT APPLICATION NUMBER: US/10-705-716A

; CURRENT FILING DATE: 2003-11-10

; PRIOR APPLICATION NUMBER: US 60/425,532

; LENGTH: 145

; TYPE: PRT

; ORGANISM: Rat

US-10-705-716A-2

Query Match 100.0%; Score 767; DB 4; Best Local Similarity 100.0%; Pred. No. 5.4e-69; Matches 145; Conservative 0; Mismatches 0

QY 1 MGCGSRADAIPEPRYESWT.....VTEINIRQMDRSKRVTKNCIN 145

Db 1 MGCGSRADAIPEPRYESWT.....VTEINIRQMDRSKRVTKNCIN 145

QY 61 SNGGVRPAAPGGIANGPEKQKNGCQCPNSQSSLSSCPRL

Db 61 SNGGVRPAAPGGIANGPEKQKNGCQCPNSQSSLSSCPRL

QY 121 EVAISVTENIRQMDRSKRVTKNCIN 145

Db 121 EVAISVTENIRQMDRSKRVTKNCIN 145

QY 121 EVAISVTENIRQMDRSKRVTKNCIN 145

Db 121 EVAISVTENIRQMDRSKRVTKNCIN 145

RESULT 2
US-10-705-716A-8

; Sequence 8, Application US/10705-716A

; Publication No. US20040146906A1

; GENERAL INFORMATION:

; APPLICANT: Robinson, John Allen

; APPLICANT: Stojanovic-Subolic, Vedrana

; APPLICANT: Babij, Philip

; APPLICANT: Murrills, Richard John

; TITLE OF INVENTION: A Novel PTH Responsive Gene

FILE REFERENCE: AML00401
; CURRENT APPLICATION NUMBER: US/10/705,716A
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: US 60/425,532
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 8
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Mouse
; US-10-705-716A-8

Query Match
Best Local Similarity 97.3%; Score 746; DB 4; Length 145;
Matches 141; Conservative 97.2%; Pred. No. 7_1e-67; Mismatches 2; Indels 0; Gaps 0;

Oy 1 MGCGGSRADAEPRYVYESWTRESTWLTYTDALPSAAADSGPAGGLAHAGVLDGP 60
Db 1 MGCGGSRADAEPRYVYESWTRESTWLTYTDALPSAAADSGPAGGLAHAGVLDGL 60

Qy 61 SSGNVLRPAPGIANPKNGTQCPNSQSLSSGSPLTOKONGLWTEAKDAKRMAR 120
Db 61 SSGNVLRPAPGIANPKNGTQCPNSQSLSSGSPLTOKONGLWTEAKDAKRMAR 120

Qy 121 EVAISVTENIRQMDRSRKVTNCIN 145
Db 121 EVAISVTENIRQMDRSRKVTNCIN 145

RESULT 3
US-10-293-239-17
; Sequence 17, Application US/10293239
; Publication No. US20030119043A1
; GENERAL INFORMATION:
; APPLICANT: Tanner, Stephan
; TITLE OF INVENTION: B4MIC expression as a diagnostic marker for acute leukemia
; FILE REFERENCE: 2272/0101
; CURRENT APPLICATION NUMBER: US/10/293, 239
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 60/318, 210
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 17
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-293-239-17

Query Match
Best Local Similarity 84.1%; Score 645; DB 4; Length 145;
Matches 121; Conservative 83.4%; Pred. No. 1e-56; Mismatches 14; Indels 0; Gaps 0;

Oy 1 MGCGGSRADAEPRYVYESWTRESTWLTYTDALPSAAADSGPAGGLAHAGVLDGP 60
Db 1 MGCGGSRADAEPRYVYESWTRESTWLTYTDALPSAAADSGPAGGLAHAGVLDGL 60

Qy 61 SSGNVLRPAPGIANPKNGTQCPNSQSLSSGSPLTOKONGLWTEAKDAKRMAR 120
Db 61 SSGNVLRPAPGIANPKNGTQCPNSQSLSSGSPLTOKONGLWTEAKDAKRMAR 120

Qy 121 EVAISVTENIRQMDRSRKVTNCIN 145
Db 121 EVAISVTENIRQMDRSRKVTNCIN 145

RESULT 4
US-10-177-390-30
; Sequence 30, Application US/0177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:

Query Match
Best Local Similarity 84.1%; Score 645; DB 4; Length 145;
Matches 121; Conservative 83.4%; Pred. No. 1e-56; Mismatches 14; Indels 0; Gaps 0;

Oy 1 MGCGGSRADAEPRYVYESWTRESTWLTYTDALPSAAADSGPAGGLAHAGVLDGP 60
Db 1 MGCGGSRADAEPRYVYESWTRESTWLTYTDALPSAAADSGPAGGLAHAGVLDGL 60

Qy 61 SSGNVLRPAPGIANPKNGTQCPNSQSLSSGSPLTOKONGLWTEAKDAKRMAR 120
Db 61 SSGNVLRPAPGIANPKNGTQCPNSQSLSSGSPLTOKONGLWTEAKDAKRMAR 120

Qy 121 EVAISVTENIRQMDRSRKVTNCIN 145
Db 121 EVAISVTENIRQMDRSRKVTNCIN 145

RESULT 5
US-10-705-716A-4
; Sequence 4, Application US/10705716A
; Publication No. US2004014696A1
; GENERAL INFORMATION:
; APPLICANT: Robinson, John Allen
; APPLICANT: Stojanovic-Suslic, Vedrana
; APPLICANT: Babij, Philip
; APPLICANT: Murrills, Richard John
; TITLE OF INVENTION: A Novel PTH Responsive Gene
; FILE REFERENCE: AML00401
; CURRENT APPLICATION NUMBER: US/10/705,716A
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: US 60/425,532
; PRIOR FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 4
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-705-716A-4

Query Match
Best Local Similarity 84.1%; Score 645; DB 4; Length 145;
Matches 121; Conservative 83.4%; Pred. No. 1e-56; Mismatches 14; Indels 0; Gaps 0;

Oy 1 MGCGGSRADAEPRYVYESWTRESTWLTYTDALPSAAADSGPAGGLAHAGVLDGP 60
Db 1 MGCGGSRADAEPRYVYESWTRESTWLTYTDALPSAAADSGPAGGLAHAGVLDGL 60

Qy 61 SSGNVLRPAPGIANPKNGTQCPNSQSLSSGSPLTOKONGLWTEAKDAKRMAR 120
Db 61 SSGNVLRPAPGIANPKNGTQCPNSQSLSSGSPLTOKONGLWTEAKDAKRMAR 120

Qy 121 EVAISVTENIRQMDRSRKVTNCIN 145
Db 121 EVAISVTENIRQMDRSRKVTNCIN 145

RESULT 6

US-10-293-239-1⁹
; Sequence 19, Application US/10293239
; Publication No. US20030119043A1
; GENERAL INFORMATION:
; APPLICANT: de la Chapelle, Albert
; TITLE OF INVENTION: B41C expression as a diagnostic marker for acute leukemia
; FILE REFERENCE: 22727/04101
; CURRENT APPLICATION NUMBER: US/10/293,239
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: US 60/348,210
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-293-239-19
Query Match 80.5%; Score 617.5; DB 4; Length 180;
Best Local Similarity 67.2%; Pred. No. 8.1e-54;
Matches 121; Conservative 10; Mismatches 14; Indels 35; Gaps 1;
Qy 1 MGCGGSRADAEIPTYVYESWTRTESTWLTYTDSDALPSAAATSGPEAGGLHA----- 53
Db 1 MGCGGSRADAEIPTYVYESWTRTESTWLTYTDSDALPSAAATSGPEAGGLHSLEAKS 60
Qy 54 -----GVLIEDCPSSNGVLRPAPPGTANPKKNGT 85
Db 61 KIKAPPTDSVSDREGLFSASKNMAPLAFLVSHGMLEDGLPSNGVPRTAPGGTPNPPEKTNCET 120
Qy 86 QCNSQSLSLSSGPLTOKONGWITTEAKDRAKMSAREVALSVTENIRQDRSKRTKGNC 145
Db 121 QCNPQPSLSSGPLTOKONGLQTEAKDRAKMRPAKEVTINVTISIQMDRDRRITKCN 180
RESULT 7
US-10-293-239-2¹
; Sequence 21, Application US/10293239
; Publication No. US20030119043A1
; GENERAL INFORMATION:
; APPLICANT: Tanner, Stephan
; TITLE OF INVENTION: B41C expression as a diagnostic marker for acute leukemia
; FILE REFERENCE: 22727/04101
; CURRENT APPLICATION NUMBER: US/10/293,239
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 60/348,210
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-293-239-21
Query Match 61.7%; Score 473.5; DB 4; Length 149;
Best Local Similarity 66.0%; Pred. No. 3e-39; Matches 95; Conservative 2; Mismatches 12; Indels 35; Gaps 1;
Qy 1 MGCGGSRADAEIPTYVYESWTRTESTWLTYTDSDALPSAAATSGPEAGGLHA----- 53
Db 1 MGCGGSRADAEIPTYVYESWTRTESTWLTYTDSDALPSAAATSGPEAGGLHSLEAKS 60
Qy 54 -----GVLEDGPSSNGVLRPAPPGTANPKKNGT 85
Db 61 KIKAPPTDSVSDREGLFSASKNMAPLAFLVSHGMLEDGLPSNGVPRTAPGGTPNPPEKTNCET 120
Qy 86 QCNSQSLSLSSGPLTOKONGWITTE 109
Db 121 QCNPQPSLSSGPLTOKONGLQTE 144
RESULT 8
US-10-705-716A-10
; Sequence 10, Application US/10705716A
; Publication No. US20040146906A1
; GENERAL INFORMATION:
; APPLICANT: Robinson, John Allen
; APPLICANT: Stojanovic-Subolic, Vedrana
; APPLICANT: Babij, Philip
; APPLICANT: Murillo, Richard John
; TITLE OF INVENTION: A Novel PRH Responsive Gene
; FILE REFERENCE: AM100401
; CURRENT APPLICATION NUMBER: US/10/705,716A
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: US 60/425,532
; PRIOR FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Mouse
; US-10-705-716A-10
Query Match 38.3%; Score 294; DB 4; Length 54;
Best Local Similarity 100.0%; Pred. No. 6.6e-22;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGCGGSRADAEIPTYVYESWTRTESTWLTYTDSDALPSAAATSGPEAGLHAG 54
Db 1 MGCGGSRADAEIPTYVYESWTRTESTWLTYTDSDALPSAAATSGPEAGLHAG 54
RESULT 9
US-10-293-239-20
; Sequence 20, Application US/10293239
; Publication No. US20030119043A1
; GENERAL INFORMATION:
; APPLICANT: Tanner, Stephan
; TITLE OF INVENTION: B41C expression as a diagnostic marker for acute leukemia
; FILE REFERENCE: 22727/04101
; CURRENT APPLICATION NUMBER: US/10/293,239
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 60/348,210
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-293-239-20
Query Match 37.5%; Score 288; DB 4; Length 73;
Best Local Similarity 91.4%; Pred. No. 3.9e-21;
Matches 53; Conservative 2; Mismatches 21; Indels 0; Gaps 0;
Qy 1 MGCGGSRADAEIPTYVYESWTRTESTWLTYTDSDALPSAAATSGPEAGGLHAGVLT 58
Db 1 MGCGGSRADAEIPTYVYESWTRTESTWLTYTDSDALPSAAATSGPEAGGLHSGLCSE 58
RESULT 10
US-10-293-239-18
; Sequence 18, Application US/10293239
; Publication No. US2003011903A1
; GENERAL INFORMATION:
; APPLICANT: Tanner, Stephan
; APPLICANT: de la Chapelle, Albert
; TITLE OF INVENTION: B41C expression as a diagnostic marker for acute leukemia
; FILE REFERENCE: 22727/04101

```

; CURRENT APPLICATION NUMBER: US/10/293,239
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 60/348,210
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 18
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-93-239-18

RESULT 11
Query Match      36.2%; Score 278; DB 4; Length 54;
Best Local Similarity 94.4%; Pred. No. 2.7e-20; Mismatches 2; Indels 0; Gaps 0;
Matches 51; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy   1 MGCGGSRADAEPRYYESWTRTESTWLTYTSDALPSAATSGPAGGLHG 54
Db   1 MGCGGSRADAEPRYYESWTRTESTWLTYTSDALPSAATSGPAGGLHG 54

RESULT 13
US-10-293-239-37
Sequence 6, Application US/10293239
Publication No. US20030119043A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, John Allen
; APPLICANT: Stojanovic-Subolic, Vedrana
; APPLICANT: Babij, Philip
; APPLICANT: Merrill, Richard John
; TITLE OF INVENTION: A Novel PRH Responsive Gene
; FILE REFERENCE: AM00401
; CURRENT APPLICATION NUMBER: US/10/705,716A
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: US 60/425,532
; PRIOR FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-705-716A-6

RESULT 12
Query Match      36.2%; Score 278; DB 4; Length 54;
Best Local Similarity 94.4%; Pred. No. 2.7e-20; Mismatches 2; Indels 0; Gaps 0;
Matches 51; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy   1 MGCGGSRADAEPRYYESTRERESTWLTYTSDALPSAATSGPAGGLHG 54
Db   1 MGCGGSRADAEPRYYESTRERESTWLTYTSDALPSAATSGPAGGLHG 54

RESULT 14
US-10-293-239-35
Sequence 35, Application US/10293239
Publication No. US20030119043A1
; GENERAL INFORMATION:
; APPLICANT: Tanner, Stephan
; APPLICANT: de la Chapelle, Albert
; TITLE OF INVENTION: B4LC expression as a diagnostic marker for acute leukemia
; FILE REFERENCE: 227704101
; CURRENT APPLICATION NUMBER: US/10/293,239
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 60/348,210
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-293-239-35

RESULT 15
US-10-767-701-48905
Sequence 48905, Application US/10767701

```

; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21 (53535)B
; CURRENT APPLICATION NUMBER: US10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 48905
; LENGTH: 147
; TYPE: PRT
; FEATURE:
; ORGANISM: Sorghum bicolor
; OTHER INFORMATION: Clone ID: LIB3476-020-PI-K1-A12.pep
US-10-767-701-48905

Query Match 12.3%; Score 94; DB 4; Length 147;
Best Local Similarity 27.5%; Pred. No. 0.32; Gaps 3;
Matches 30; Conservative 17; Mismatches 52; Indels 10; Gaps 3;
Qry 36 LPSIAATSGPAGGLHAGVLEDPSSNVRKRPAPGIANPKRNGTCCNSQS-- 92
Db 29 LPALALPDAGALEGADNGGAHRGPHRG---QERAGAGARQALHCOPCPHSIDSCIG 84
Qry 93 -LSSGPLTOKO-NGLWTTTEAKDAKRMSSAREVAISVTENIROMDRSKR 138
Db 85 RWISIGTSGHRPCSGLLSVQLRQMPRSSAAQRKEIKQIQEORRVR 133

Search completed: May 20, 2006, 21:23:19
Job time : 75 secs


```

; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 2428
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-511-937-2428

Query Match 8.4%; Score 64.5; DB 6; Length 413;
Best Local Similarity 24.2%; Pred. No. 6.3; Mismatches 12; Indels 32; Gaps 2;
Matches 23; Conservative 12; Mismatches 25; Indels 35; Gaps 4;

Qy 63 NGSLRPRAPGGIANPEKHN--NCGTQCPNSL-----SSG----- 96
Db 235 NCQNRP---LIRPKKLIVSKRAGQCTINOTTITLWRUNASGDPPVCNAAGLYKLH 289

Qy 97 ---PLTOKONGIWTTEAKRDKARMSAREVAISVT 127
Db 290 QNRPLTRKQJOTRNKRSKGGKKGSSNLG3T 324

RESULT 3
US-10-370-959-131

; Sequence 131, Application US/10370959
; Publication No. US20060088907A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Williamson, Mark W.
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: MacBeth, Kylie J.
; APPLICANT: Hunter, John J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Bandaru, Rajasekhar
; APPLICANT: Tai, Fong-Ying
TITLE OF INVENTION: NOVEL 1237, 18480, 2245, 16228, 7677, 21617, 55562, 39228, TITLE OF INVENTION: 28320, 46619, 33166, 16836, 46807, 21657, 52155, 32229, 22325, 46863 AND TITLE OF INVENTION: 3225, MOLECULES AND USES THEREFOR
FILE REFERENCE: MP103-017OMNM
CURRENT APPLICATION NUMBER: US/10/370,959
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: US 09/910,150
PRIOR FILING DATE: 2001-07-18
APPLICATION NUMBER: US 6/0/219,028
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: US 10/251,507
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: US 09/715,479
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: US 6/0/218,053
PRIOR FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: US 09/544,929
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: US 6/0/212,439
PRIOR FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 09/592,870
PRIOR FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: US 6/0/214,174
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 09/775,117
PRIOR FILING DATE: 2000-02-01
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 156
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 131
LENGTH: 262
TYPE: PRT

; ORGANISM: Artificial sequence
; FEATURE: OTHER INFORMATION: Consensus amino acid sequence
; US-10-370-959-131

Query Match 8.3%; Score 64; DB 6; Length 262;
Best Local Similarity 24.7%; Pred. No. 3.8; Mismatches 32; Indels 20; Gaps 2;
Matches 20; Conservative 9; Mismatches 32; Indels 20; Gaps 2;

Qy 110 AKRDAKRMSAREVAISVT 130
Db 95 APAARGNPQVLEKSLKGPKHIEYQVLADHGNCITLCNRACSDORGIRTRQSIEVAPSQ 154

RESULT 4
US-11-301-554-1812
; Sequence 1812, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Barrick
; APPLICANT: Sleath, Paul R.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedula, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY OF LUNG CANCER
FILE REFERENCE: 210121.478221
CURRENT APPLICATION NUMBER: US/11/301,554
CURRENT FILING DATE: 2005-12-13
PRIOR APPLICATION NUMBER: US 10/283,017
PRIOR FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: US 10/113,872
PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 10/017,754
PRIOR FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: US 09/902,941
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 09/849,626
PRIOR FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: US 09/736,457
PRIOR FILING DATE: 2000-12-13
PRIOR APPLICATION NUMBER: US 09/702,705
PRIOR FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: US 09/677,419
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: US 09/671,325
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/658,824
PRIOR FILING DATE: 2000-09-08
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2157
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 1812
LENGTH: 474
TYPE: PRT

; ORGANISM: Homo sapiens
; US-11-301-554-1812

Query Match 8.3%; Score 64; DB 7; Length 474;
Best Local Similarity 24.5%; Pred. No. 8.6; Mismatches 7; Indels 27; Gaps 3;
Matches 26; Conservative 7; Mismatches 27; Indels 46; Gaps 3;

```

RESULT 5
US-10-511-937-2464
; Sequence 2464, Application US/10511937
; Publication No. US20060088836A1
GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: FRY, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James B
; APPLICANT: Morris, Macdonald
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIORITY APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 2464
; LENGTH: 443
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-511-937-2464

RESULT 6
US-10-505-928-784
; Sequence 784, Application US/10505928
; Publication No. US2006008852A1
GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/391B
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; LENGTH: 2671
; TYPE: PRT
; ORGANISM: Homo sapiens

RESULT 7
US-11-251-465-23
; Sequence 23, Application US/11251465
; Publication No. US2006004061A1
GENERAL INFORMATION:
; APPLICANT: BRYB, Reginald
; APPLICANT: Vandeginste, Nick
; APPLICANT: Tomme, Peter
; APPLICANT: Klaassen, Robertus
; TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
; TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And
; TITLE OF INVENTION: Inflammatory Diseases
; FILE REFERENCE: P30, 172-A USA
; CURRENT APPLICATION NUMBER: US/11/251,465
; CURRENT FILING DATE: 2005-10-14
; PRIORITY APPLICATION NUMBER: 60/619,384
; PRIOR FILING DATE: 2004-10-15
; NUMBER OF SEQ ID NOS: 880
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 23
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-251-465-23

RESULT 8
US-10-322-836-43
; Sequence 48, Application US/10322836
; Publication No. US20060090212A1
GENERAL INFORMATION:
; APPLICANT: Turner, Alexander C., Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Neils, Michael
; APPLICANT: Friedrich, Glenn A.
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
; TITLE OF INVENTION: ENCODED THEREBY
; FILE REFERENCE: 8335-0037-999
; CURRENT APPLICATION NUMBER: US/10/322,836
; CURRENT FILING DATE: 2002-12-18
; PRIORITY APPLICATION NUMBER: US/09/579,114
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentSEQ for Windows Version 3.0
; SEQ ID NO: 48

Query Match 8.1%; Score 62; DB 6; Length 2671;
Best Local Similarity 29.3%; Pred. No. 1.5e+02;
Matches 27; Conservative 16; Mismatches 33; Indels 16; Gaps 7;

QY 47 ---EAGGHHAGVLEDGSSNSNGVTPAAGGTIAN-PERKMQCGTQ 86
Db 157 KVGGSSGGGGGGSSNAGGGGASGGGANSKPAOKSCG 202

QY 54 GLVBDGPSSNGVTPAAGGTIANPEKRM-NCIGQ-CP-NQSLSGSPLOXQNGLWTEA 110
Db 30 GLVDD---RCVTPA-GDLDPKKRDRUDLFLPKCPMRS-----AQKQ-YMKAKQ 76

QY 111 KRDAMSRAREAVTSVNTIRDRSKRTVN 142
Db 77 TKQDKEKLAADVILQKLOHRAHQEQKQDTE 108


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; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 458
; LENGTH: 734
; ORGANISM: Homo sapien
; US-10-196749-458

Query Match          7.8%; Score 59.5; DB 6; Length 734;
Best Local Similarity 30.4%; Pred. No. 48; Mismatches 27; Indels 13; Gaps 5;
Matches 24; Conservative 15; Mismatches 27; Indels 13; Gaps 5;

Qy      33 SDALPSAATDS--GPEAG--GLHAGVIEDGPSNGVLRPAAPGGIANPEKKGKNCGTQC 87
Db      126 SDPRLSEASSOSSFGLGPHGRGLNHSGLG--LEDGDYDGM--CAEQDADPWFQVDAG-- 179
Qy      88 PNSCSSLSSCPLTOKHGLW 106
Db      180 -HPTRPSCVITQGRNSVW 196

RESULT 12
US-10-538-056-363

; Sequence 363, Application US/10538066
; Publication No. US20060094649A1
; GENERAL INFORMATION:
; APPLICANT: Biimmune Inc.
; TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen
; FILE REFERENCE: 2060_015PC06
; CURRENT APPLICATION NUMBER: US/10/538,066
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/432,017
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 757
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 363
; LENGTH: 702
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-538-056-363

RESULT 13
US-10-505-928-831

; Sequence 831, Application US/10505928
; Publication No. US2006008532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 2867/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 831
; LENGTH: 2026
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-505-928-831

RESULT 14
US-11-169-140-14

; Sequence 14, Application US/11169140
; Publication No. US20060099150A1
; GENERAL INFORMATION:
; APPLICANT: ARIZEKE PHARMACEUTICALS, INC.
; APPLICANT: HOUSTON, Lou, L.
; APPLICANT: SHERIDAN, Philip, J.
; APPLICANT: HAWLEY, Stephen
; APPLICANT: GLINN, Jacqueline, M.
; APPLICANT: CHAPIN, Steven
; TITLE OF INVENTION: METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE AGENTS ACROSS C
; FILE REFERENCE: 11474-037-959
; CURRENT APPLICATION NUMBER: US/11/169,140
; CURRENT FILING DATE: 2005-06-27
; PRIOR APPLICATION NUMBER: US 60/267,601
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/248,819
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/248,478
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US 60/237,929
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/949,039
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: 09/969,748
; PRIOR FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.0
; ORGANISM: Homo sapiens
; US-11-169-140-14

Query Match          7.7%; Score 59; DB 6; Length 2026;
Best Local Similarity 27.8%; Pred. No. 2e+02; Mismatches 32; Indels 26; Gaps 7;
Matches 27; Conservative 12; Mismatches 32; Indels 26; Gaps 7;

Qy      2 GGCGSRAADAEPRPVYESWRETES-TWYTYSDALISSAATSGPENGGIHLAVLREGP 60
Db      798 GVGGLRCRRCRGCFWNFRGIVDRGSGCPSCD--PGCAVVRDCCBOMGLC----- 848
Qy      61 SSNGVLRPAPGGIANPEKKGKNCGTQFNPNSLSSGP 97
Db      849 -----CRP---GVAGK---CG-QEFGRAL--GP 869

RESULT 15
US-10-505-928-831

; Sequence 831, Application US/10505928
; Publication No. US2006008532A1
; GENERAL INFORMATION:
; APPLICANT: ARIZEKE PHARMACEUTICALS, INC.
; APPLICANT: HOUSTON, Lou, L.
; APPLICANT: SHERIDAN, Philip, J.
; APPLICANT: HAWLEY, Stephen
; APPLICANT: GLINN, Jacqueline, M.
; APPLICANT: CHAPIN, Steven
; TITLE OF INVENTION: METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE AGENTS ACROSS C
; FILE REFERENCE: 11474-037-959
; CURRENT APPLICATION NUMBER: US/11/169,140
; CURRENT FILING DATE: 2005-06-27
; PRIOR APPLICATION NUMBER: US 60/267,601
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/248,819
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/248,478
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US 60/237,929
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/949,039
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: 09/969,748
; PRIOR FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.0
; ORGANISM: Homo sapiens
; US-10-505-928-831

Query Match          7.7%; Score 59; DB 6; Length 702;
Best Local Similarity 18.5%; Pred. No. 51; Mismatches 67; Indels 58; Gaps 9;
Matches 36; Conservative 34; Mismatches 67; Indels 58; Gaps 9;

Qy      6 SRADAEPRPVYESWRETE--STWLTYDSDALP-----SAATSG 45
Db      330 NSNSNPVERBDAVALTCEPIQNTYIWWNNQSPLVSPIQLSNDNRITLISVTRDVG 389
Qy      46 PEAGGLHAGVLT-----GPSENGVLPA---APG-----GIANPEKKGK 82
Db      390 PYEGGIONBLSVDHSDPVLNVLYGP--DOPTRISPYTYRPGVNLISCHAASNPQAQY 448

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; SEQ ID NO 14
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; US-11-169-40-14

Query Match 7.6%; Score 58.5, DB 7; Length 663;
Best Local Similarity 24.0%; Pred. No. 54; Mismatches 31; Indels 15; Gaps 1;
Matches 18; Conservative 11; Mismatches 31; Indels 15; Gaps 1;

QY      38 SAAATSGPEAGCILHAGVLEDGPSSNGVLRPAAPGIANPEKKNCGTQCPNSQSLSGP 97
Db      211 NWATSDOCKPKRAKRGV-----PGELATPDKENDAKSSDSSVGEBTLP 255
QY      98 L'OKONGWTTBKR 112
Db      256 SSILSKSGKVKVDAEK 270

RESULT 15
US-10-505-928-569
; Sequence 569, Application US/10505928
; Publication No. USC0060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 2896739178
; CURRENT APPLICATION NUMBER: US/10/505, 928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363, 019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 569
; LENGTH: 4590
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-505-928-569

Query Match 7.6%; Score 58.5, DB 6; Length 4590;
Best Local Similarity 21.6%; Pred. No. 7.4e+02; Mismatches 27; Indels 19; Gaps 5;
Matches 27; Conservative 23; Mismatches 56; Indels 19; Gaps 5;

QY      22 ETEST---WLTV--TDSALPAA-----ATSGPEAGG--LHAGVLEDGPSSNG 64
Db      1098 DRETSIHWLTFATDQGVVPHSSPIEYIEWEDVNINAQSEPVVYPEIENNSPKDVS 1157
QY      65 VVPAAMGGIAMPBEKKNGTCOPNSQSLSSPLTQKONGLWTEAKRDAKMSAREVAT 124
Db      1158 VVQIEAFDPDSSNDKLMVKTISGNPOQFFS--IHPKTGLITISRKLDRQQDEHLEV 1215
QY      125 SYTEN 129
Db      1216 TTYDN 1220

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Search completed: May 20, 2006, 21:23:46
 Job time : 5 secs

A:Map position: 13R
 A:Residues: transmembrane protein
 C:Keywords: transmembrane #status predicted <TM1>
 A:Cross-references: UNIPARC:UPI0000168DC; EMBL:X94215; NID:91122900; PIDN:CAA63906.1;
 C:Genetics:
 A:Gene: SGD:CAT8; MSBP
 A:Cross-references: SGD:S000493; MIPS:YMR280C
 C:Keywords: transmembrane protein
 C:Species: *Streptomyces coelicolor*
 C:Accession: T31073
 C:Date: 03-Dec-1999 #text_change 09-Jul-2004
 R.Sanders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.
 submitted to the EMBL Data Library, August 1999
 A:Reference number: 221621
 A:Accession: T31073
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Residues: 1-269 <SAN>
 A:Cross-references: UNIPROT:Q8Y13; UNIPARC:UPI00000DC600; EMBL:ALI10973; PIDN:CAE53307
 A:Experimental source: strain A3 (2)
 C:Genetics:
 A:Gene: SCORBB:SCJ30_06c

RESULT 5

Query Match	Score	DB	Length
Best Local Similarity	10.8%	2	1433;
Matches	29.4%	Pred.	No. 20;
		Mismatches	50;
		Indels	12;
		Gaps	4;

Qy 36 LPSAATTDGSPERAGGLIAGVLDGPSNSVLRPAAPGGIANPEKKKNGTQCPNSLSS 95
 Db 927 LPATTTSILKEPLGSQSKNSLNQRQTPNVR-----ENPEHEVYGNDSNNNNSEA 979
 Qy 96 G---PLTKKONGLWTTTEAKRDAAKMSRAEVAVSYTENIR--DMDRSKV 140
 Db 980 GHSPMTNTNGNKRLYKEDAK-NAKDGGISKGEMAHNFONDTKKMS 1027

RESULT 6

Query Match	Score	DB	Length
Best Local Similarity	10.6%	2	269;
Matches	26.8%	Pred.	No. 4.5;
		Mismatches	38;
		Indels	24;
		Gaps	4;

Qy 11 IIPRYYSWTT-----RETESTWLTYTDALPSAATTDGSPERAGGLIAGVLDGPS 60
 Db 176 LPPTHWQEWQWPVNPHCRPRRRVRLSSEGTFSPSTVLPSPRGCCGSGERTGG----- 225
 Qy 61 SSGNGURPAPEGIANPEKOMCG-TQCPNSQSLSS 95
 Db 226 -GGGVVTTGAGGGIV-PGAAACRGCGRAHAMPTNSRS 260

A:Accession: S66852
 A:Species: *Saccharomyces cerevisiae*
 A:Alternate names: hypothetical protein YOL155c - yeast (*Saccharomyces cerevisiae*)
 C:Accession: 12-Jul-1996 #Sequence_revision 12-Jul-1996 #text_change 09-Jul-2004
 R.Arino, J.; Casamayor, A.; Gano, P.J.; Gancedo, C.; Lafuente, M.J.; Aldea, M.; Casas,
 submitted to the Protein Sequence Database, July 1996
 A:Reference number: S66814
 A:Accession: S66852
 A:Molecule type: DNA
 A:Residues: 1-967 <ARL>
 A:Cross-references: UNIPROT:Q88294; UNIPARC:UPI00006C5C2; EMBL:Z74897; NID:9140063; F
 A:Experimental source: strain S288C
 R.Gaillou, L.; Dujon, B.

submitted to the Protein Sequence Database, July 1996

A;Reference number: S66854

A;Molecule type: DNA

A;Residues: 1-167 <GAI>

A;Experimental source: brain S288C

R;Gamo, F.J.; Lafuente, M.J.; Casamayor, A.; Aldea, M.; Casas, C.; Ario, J.; Herrero, E.

submitted to the EMBL Data Library, July 1995

A;Description: Analysis of the DNA sequence of a 15500 bp fragment of the left arm of ch

pen reading frames.

A;Reference number: S67324

A;Accession: S67325

A;Molecule type: DNA

A;Residues: 1-164, 'STSTGGSSATGGSGSISATGGSSAGSS', 166-186, 'V', 188-967 <GAM>

A;Cross-references: UNIPARC:UPI00006C5C2; EMBL:Z74897; NID:91420063; PID:e251930; PID:q

R;Gamo, F.J.; Lafuente, M.J.; Casamayor, A.; Arino, J.; Aldea, M.; Casas, C.; Herrero, E.

Yeast 12, 709-711, 1995

A;Title: Analysis of the DNA sequence of a 15,500 bp fragment near the left telomere of

and two new open reading frames.

A;Accession: S70380

A;Reference number: S70379; MUID:96405919; PMID:881004

A;Status: nucleic acid sequence not shown

A;Map position: SGD:S0005515

A;Note: YOL15C

Query Match 10.6%; Score 81; DB 2; Length 967;

Best Local Similarity 24.8%; Pred. No. 20; Mismatches 29; Conservative 23; MisMatches 55; Indels 10; Gaps 2;

A;Accession: Q9Y

17 ESMRPRETESTWLTVDSDAHLRSAAITDSDPERRG---IHNQVLEDPSGSVLRPAFG 72

A;Accession: Q9Db

182 ESGSSAGSSGSSATESGSSVGSSSATESGSSGSSATESGSSASSPVSSGSVTEGES 241

A;Accession: Q9QY

73 GIANIEKKKNGTQCPNSOSSLSSGSPILTKONGLWTTAEAKDKRMSAREVAISVTEN 129

A;Accession: Q9Db

242 SSASISSITQSGTACGSSSSATSSGTVQSGSSVGSSSA-----SAPGISSIPQS 292

A;Accession: Q9Db

RESULT 7

A;Accession: T09144

probable guanine nucleotide exchange factor RhoGDP2 - fruit fly (*Drosophila melanogaster*)

C;Species: *Drosophila melanogaster*

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

A;Accession: T09144; T09223

R;Haecker, U.; Perrimon, N. Library, submitted to the EMBL Data Library, October 1997

A;Reference number: Z16586

A;Accession: T09144

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: mRNA

A;Residues: 1-2259 <HAE>

A;Cross-references: UNIPROT:044113; UNIPARC:UPI00007F684; EMBL:AF031930; NID:92687355;

R;Barrett, K.; Lepin, M.; Settleman, J.

A;Title: The Rho GTPase and a putative RhoGDP mediate a signaling pathway for the cell

A;Reference number: Z16618; MUID:98088790; PMID:9428514

A;Accession: T09223

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: mRNA

A;Residues: 1-676, 'L', 678-837, 'L', 839-889, 'S', 891-1233, 'D', 1245-1338, 'E', 1360-1368, 'R', 1

A;Cross-references: UNIPARC:UPI00007D45E; EMBL:AF032870; NID:92760367; PID:NAC38820.1;

C;Genetics:

A;Gene: rhoGFR2

A;Cross-references: FlyBase:FBgn0023172

A;Map position: 2; 53F1-2

A;Note: orchestrates cell shape changes during gastrulation

C;Function:

A;Description: mediates actin rearrangements required for cell shape changes during ga

C;Superfamily: rat Munc-13-3 protein; protein kinase C zinc-binding repeat homology

R;1151-1200/Domain: protein kinase C zinc-binding repeat homology <K2N>

Query Match 10.4%; Score 79.5; DB 2; Length 2559;

Best Local Similarity 28.3%; Pred. No. 83; Mismatches 30; Conservative 11; MisMatches 56; Indels 9; Gaps 3;

A;Accession: Q9Y

5 GSRADAIERPIVYESWREERSTWLTVDSDALPSAAMTSGPBRAGLHQAVLEDPSSNG 64

A;Accession: Q9Db

799 GSSPDNMHPHRPHDRITKTTSQSW-EIVRKEDGESEPPGTTPPPVLSHMTVLEDPNENN 857

A;Accession: Q9QY

65 VLRLPAPG-GIANIEKKKNGTQCPNSOSSLSSGSPILTKONGLWTTAEAKDKRMSAREVAISVTEN 102

A;Accession: Q9Db

858 GAAAGCPGVIESHOFTPMAGASSPIPISPLSHNINHAQSNDTQE 903

A;Accession: Q9Db

RESULT 8

A;Accession: A40670

Query Match 10.4%; Score 79.5; DB 2; Length 2559;

Best Local Similarity 28.3%; Pred. No. 83; Mismatches 30; Conservative 11; MisMatches 56; Indels 9; Gaps 3;

A;Accession: A40670

nuuclear envelope protein POM 121 - rat

C;Species: *Rattus norvegicus* (Norway rat)

C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004

R;Hallberg, E.; Wozniak, R.W.; Blobel, G.

J;Cell Biol. 122, 513-521, 1993

A;Title: An integral membrane protein of the pore membrane domain of the nuclear envelop

A;Reference number: A40670; MUID:93320754; PMID:8335683

A;Accession: A40670

A;Status: preliminary

A;Map position: SGD:S0005515

A;Accession: Q9Db

1-119 <HAL>

A;Cross-references: UNIPROT:P52591; UNIPARC:UPI000012FC0B; GB:Z21513; NID:9396746; PID:F083-807, 845-849, 956-960, 1010-1014, 1047-1051, 1076-1080/Region: pentapeptide motif (X-)

Query Match 10.2%; Score 78.5; DB 2; Length 1199;

Best Local Similarity 25.2%; Pred. No. 43; Mismatches 39; Conservative 19; MisMatches 56; Indels 41; Gaps 6;

A;Accession: Q9Db

20 TREPSTWLTVDSDALPSA--AATDGPPEAGLHAASVLEDPSSNGSVLRPAPGGIA- 75

A;Accession: Q9Db

363 SRTSVSSVSLSTCGPGSSRNNAITSSYSTRGSVQSWLRSKPTSSPPSPASSRSP 422

A;Accession: Q9Db

423 ERPAKTR--ERPRHQSSSAPIVTDKPSGKVTDATGKQSLWTSPPGCRK 480

A;Accession: Q9Db

76 -NPRAKKGTOCPNSOSSLSSGEL-----TOKONGLWTT-----BAK 111

A;Accession: Q9Db

112 RDAKRMSA-----EVASVTHNIRODR 135

A;Accession: Q9Db

481 RKLQIUPSPRRGDQLTLPPPELGYSITADELDMER 515

A;Accession: Q9Db

RESULT 9

A;Accession: T09225

A;Kinase anchor protein AKAP-KL isoform 1 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C;Accession: T09225; T09226; T09227

R;Bong, F.; Feldmesser, M.; Casdevall, A.; Rubin, C.S.

J;Biol. Chem. 273, 6533-6541, 1998

A;Title: Molecular characterization of a cDNA that encodes six isoforms of a novel mur

A;Reference number: 216620; MUID:98165844; PMID:9497389

A;Accession: T09225

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: mRNA

A;Residues: 1-885 <DO>

A;Cross-references: UNIPROT:054931; UNIPARC:UPI000028356; EMBL:AF033274; NID:92852696;

C;Genetics:

A;Gene: rhoGFR2

A;Cross-references: FlyBase:FBgn0023172

A;Map position: 2; 53F1-2

A;Note: orchestrates cell shape changes during gastrulation

A;Cross-references: UNIPARC:UPI00002438B; EMBL:AE032275; NID:92852698; PID:92852699	A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallo, M.; Ichijo, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holzapfel, S.; Hosono, S.; Hull, M.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurata, K.; Lapius, J.; Lardinois, A.; Authors: Lauber, J.; Lazarovic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maejee, A.; Status: preliminary; translated from GB/EMBL/DBJ
A;Residues: 1-789; PSIGST' <D03>	A;Note: binds the regulatory subunits (RII) of protein kinase Akt isoforms
A;Gene: AKAP-KU	A;Cross-references: UNIPARC:UPI000027DD; EMBL:AF033276; NID:92852700; PID:92852701
C;Keywords: alternative splicing; kidney; lung; signal transduction	A;Note: binds the regulatory subunits (RII) of protein kinase Akt isoforms
RESULT 10	Query Match 10.2%; Score 78; DB 2; Length 885; Best Local Similarity 29.6%; Pred. No. 33; Matches 34; Conservative 16; Mismatches 33; Indels 32; Gaps 7; A;Status: preliminary; nucleic acid sequence not shown; translation not shown
Qy 49 GGILRAGVLEDPGSSNGVLRPAAPGGI-----ANPEKKKNCGTCOPNQNSLSGGP---L 98	A;Molecule type: DNA
Db 381 GSRS---DKPPT---ILMPATVGGTLEDGSGTQAKEQKAPCVCSE--SOSAGCQPNAA 431	A;Residues: 1-600 <KUN>
Oy 99 TQKONGLWTTAEKR-----DAKRMASAREVALSVTEN---IROMDRSKRV 140	A;Cross-references: UNIPROT:034330; UNIPARC:UPI0000604E9; GB:Z99114; GB:AL009126; NID:169580; MUID:98044033; PMID:9384377
Db 432 TQKGRGPYSEPSKRGPLSKLWAEDCETSAARAVLTWVKOEDHGLIDQFSRSVNV 486	A;Experimental source: strain 168
A;Status: preliminary; translated from GB/EMBL/DDBJ	A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Molecule type: DNA	A;Gene: yobI
A;Residues: 1-3488 <FUL>	A;Cross-references: uncharacterized conserved protein
A;Experimental source: strain Bristol N2; clone P12F3	A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Genetics: CESP:P12F3_3	A;Molecule type: DNA
A;Map position: 5	A;Residues: 1-600 <KUN>
A;Introns: 281/3; 332/1; 562/3; 600/3; 1866/3; 1944/3; 3393/1	A;Cross-references: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis
Query Match 10.2%; Score 78; DB 2; Length 3488; Best Local Similarity 23.1%; Pred. No. 1.6e+02; Matches 33; Conservative 23; MisMatches 3; Gaps 7; A;Status: preliminary; translated from GB/EMBL/DDBJ	A;Reference number: T34418
Qy 9 DAIEPRYYEWTR-----TESTWLTYTDSDALPSAAMTDSPGERAGGLHAGVLDEGPS 61	A;Accession: T34418
Db 342 DAISAAIESTSYQDMVNGDAYSRSRWVY---AIGSVAVAVGVTGK---AGAINKADA 393	R;Fulton, B.; Wohlmann, P.
Qy 62 SINGVRLPAACGIA-----NPEKKKNCGQCPNQNSLSGGP---NSQSLSSQPLT----- 99	R;Submitter: to the EMBL Data Library, July 1998.
Db 394 AGKVINKASDGKKTIDVKIIPDPLYPNPKVTLADNPVNPVNDSONLKLNTACKIP 453	A;Description: The sequence of C. elegans cosmid P12F3.
Oy 100 -----OKQONGLWTTAEKRDAKRMASAREVALSVTENIRQMDRSKV 139	A;Accession: T34418
Db 454 DGTRKPTGQKSPPLANKKED---ANIEEGKVKAGKVKDVSRRV 497	A;Gene: P12F3
RESULT 11	Query Match 9.9%; Score 76; DB 2; Length 645; Best Local Similarity 31.0%; Pred. No. 35; Matches 31; Conservative 12; MisMatches 31; Indels 26; Gaps 4; A;Status: preliminary; nucleic acid sequence not shown; translation not shown
Qy 24 ESTWIL-TYTDSDALPSAAMTDSPGERAGGLHAGVLDEGPSNGVLRPAAPGGI 76	A;Molecule type: DNA
Db 2772 DSDWELIANTIDRNKEFKRSITESGQYVQWTGTHA-----VSSPSEETN 2817	A;Residues: 1-645 <SAU>
Oy 77 PEKQKNGCTQCPNSQSLSSCPRLTQIOKQONGLWTTAEKRDAKRMASAREVAL-----S 125	A;Cross-references: UNIPROT:P28286; UNIPARC:UPI000124F41; EMBL:Z11490; NID:97506; PID:92155185; PMID:1310937
Db 2818 PVKULIVPGSMPASK-----TECK---TDAAKSESEOKSAEELVAEKQVDQGQSASES 2866	A;Gene: FlyBase:5-km1B
Oy 126 VTEINRQMRSKRTK 141	A;Cross-references: FlyBase:FBgn0004572
Db 2867 TTEAVEE-KTCKKVTK 2831	A;Gene: FlyBase:FBgn0004572
RESULT 11.	A;Cross-references: FlyBase:FBgn0004572
C;Species: Bacillus subtilis	C;Superfamily: octopamine receptor type I
C;Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein	F;124-145/Domain: transmembrane #status predicted <TM1>
C;Residues: 1-214; Domain: transmembrane #status predicted <TM2>	F;156-177/Domain: transmembrane #status predicted <TM2>
C;Cross-references:	F;193-214/Domain: transmembrane #status predicted <TM3>
C;Genetics:	F;234-256/Domain: transmembrane #status predicted <TM4>
C;Gene: FlyBase:5-km1B	F;281-305/Domain: transmembrane #status predicted <TM5>
C;Cross-references:	F;567-587/Domain: transmembrane #status predicted <TM6>
C;Species: Bacillus subtilis	F;597-619/Domain: transmembrane #status predicted <TM7>
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Oct-2004	Query Match 9.9%; Score 76; DB 2; Length 645; Best Local Similarity 31.0%; Pred. No. 35; Matches 31; Conservative 12; MisMatches 31; Indels 26; Gaps 4; A;Status: preliminary; translated from GB/EMBL/DBJ
C;Accession: C69899	A;Cross-references: FlyBase:FBgn0004572
R;Kunst, F.; Ogasawa, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chodat, E.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Nature 249, 266-276, 1997	A;Gene: FBgn0004572
Nature 249, 266-276, 1997	Qy 29 TYTDSDALPSAAMTDSPGERAGGLHAGVLDEGPSNGVLRPAAPGGI-----IANPEKKNGC 84

Db	489 TTPSEKALSGAGTVAGAVAGVAGSGSGSGSGSGGGAGTGGKNAVGVLGCGVLAISANPHQKL-- 545	Qy	13 PRYESWTRTESTIWLTIVTDSDLAPSAAATDSPPRAGGLHAGVLEDGPGSSNGVLRPAAPG 72
Oy	85 TQCPNSQSLSSGPLTOKQNGIWTTEAKRDARKMSAREVAL 124	Db	77 PSQGNSPPEQESQLTWTGP-----AHQGPFEGPFF---WKDEBEBAMEL--- 118
Db	546 -----AKRQL-L-EAKRE-RKAQTAI 566	Qy	73 GIANPEKQKNCQCPNSQSLSSGPLTOKQNGIWTTEAKRDARKMSAREVA-SVTENR 131
RESULT 13		Db	119 GLKDPEE---GILPFSQSLSBPFPVQBEENPQRMANPGIKCPAVTSIGNVEMTERBL 174
E84824	hypothetical protein At2g40040 [imported] - Arabidopsis thaliana	Qy	132 QMRSKRVTKNCI 144
C;Species: Arabidopsis thaliana (mouse-ear cress)	C;Accession: E84824	Db	175 APGRSSVAVNNCI 187
R;Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;	C;Accession: E84824	Qy	133 PRYEWTRTESTIWLTIVTDSDLAPSAAATDSPPRAGGLHAGVLEDGPGSSNGVLRPAAPG 72
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayan, L.; Talton, J.	C;Accession: E84824	Db	77 PSQGNSPPEQESQLTWTGP-----AHQGPFEGPFF---WKDEBEBAMEL--- 118
Nature 402, 761-768, 1999	A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.	Qy	73 GIANPEKQKNCQCPNSQSLSSGPLTOKQNGIWTTEAKRDARKMSAREVA-SVTENR 131
A;Reference number: A84420; MUID:20083487; PMID:10617197	A;Accession: E84824	Db	119 GLKDPEE---GILPFSQSLSBPFPVQBEENPQRMANPGIKCPAVTSIGNVEMTERBL 174
A;Status: preliminary	A;Molecule type: DNA	Qy	132 QMRSKRVTKNCI 144
A;Residues: 1-839 <STO>	A;Cross-references: UNIPROT:004207; UNIPARC:UPI0000AB62E; GB:AE002093; NID:92088657; PI	Db	175 APGRSSVAVNNCI 187
C;Genetics:	A;Gene: At2g40040	Qy	133 PRYEWTRTESTIWLTIVTDSDLAPSAAATDSPPRAGGLHAGVLEDGPGSSNGVLRPAAPG 72
A;Map position: 2	C;Accession: E84824	Db	77 PSQGNSPPEQESQLTWTGP-----AHQGPFEGPFF---WKDEBEBAMEL--- 118
Query Match 9.9%; Score 76; DB 2; Length 839;	Best Local Similarity 23.8%; Pred. No. 48; Mismatches 62; Indels 52; Gaps 6;	Qy	133 PRYEWTRTESTIWLTIVTDSDLAPSAAATDSPPRAGGLHAGVLEDGPGSSNGVLRPAAPG 72
Matches 40; Conservative 14; Mismatches 62; Indels 52; Gaps 6;	Db	77 PSQGNSPPEQESQLTWTGP-----AHQGPFEGPFF---WKDEBEBAMEL--- 118	
Oy	5 GSRADATEPRYYESWTR-----ETESTWLTYDSDALPSAA----- 41	Qy	133 PRYEWTRTESTIWLTIVTDSDLAPSAAATDSPPRAGGLHAGVLEDGPGSSNGVLRPAAPG 72
Db	338 GSGAIVLG-----WNKKSESETESGATGQSSDKTKSGARAWNSWDKGKNIETDSEPAWG 392	Db	77 PSQGNSPPEQESQLTWTGP-----AHQGPFEGPFF---WKDEBEBAMEL--- 118
Oy	42 -----TDSGPERAGGL-----HAGVLEDGPSNSCV-----LRAAAPGCTANPEKPM 81	Qy	133 PRYEWTRTESTIWLTIVTDSDLAPSAAATDSPPRAGGLHAGVLEDGPGSSNGVLRPAAPG 72
Db	393 SQGKKNSETESTGPAWGAWDKKKSBTEPGPAGWNGDKKNSTELGPAAMGNDKKKSDT 452	Db	77 PSQGNSPPEQESQLTWTGP-----AHQGPFEGPFF---WKDEBEBAMEL--- 118
Oy	82 NCCTQCPNSQSLSSGPLTOKQNGIWTTEAKRDARKMSAREVAISVTEN 129	Qy	133 PRYEWTRTESTIWLTIVTDSDLAPSAAATDSPPRAGGLHAGVLEDGPGSSNGVLRPAAPG 72
Db	453 KSGPAAWSSTDAAWGSDDKNN-----SETESDAAWGSRNKTKSEIES 496	Db	77 PSQGNSPPEQESQLTWTGP-----AHQGPFEGPFF---WKDEBEBAMEL--- 118
RESULT 14		Qy	133 PRYEWTRTESTIWLTIVTDSDLAPSAAATDSPPRAGGLHAGVLEDGPGSSNGVLRPAAPG 72
S22571	Integrase-like protein FE65 - rat	Db	77 PSQGNSPPEQESQLTWTGP-----AHQGPFEGPFF---WKDEBEBAMEL--- 118
C;Species: Rattus norvegicus (Norway rat)	C;Accession: S22571; S22572	Qy	133 PRYEWTRTESTIWLTIVTDSDLAPSAAATDSPPRAGGLHAGVLEDGPGSSNGVLRPAAPG 72
C;Date: 31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004	R;Duilio, A.; Zambrano, N.; Mogavero, A.R.; Ammendola, R.; Cimino, F.; Russo, T.	Db	77 PSQGNSPPEQESQLTWTGP-----AHQGPFEGPFF---WKDEBEBAMEL--- 118
A;Residues: S22571; MUID:92020215; PMID:1923810	Nucleic Acids Res 19, 5269-5274, 1991	Qy	133 PRYEWTRTESTIWLTIVTDSDLAPSAAATDSPPRAGGLHAGVLEDGPGSSNGVLRPAAPG 72
A;Molecule type: mRNA	Arf1: A rat brain mRNA encoding a transcriptional activator homologous to the DNA binding protein	Db	77 PSQGNSPPEQESQLTWTGP-----AHQGPFEGPFF---WKDEBEBAMEL--- 118
A;Residues: 1-499 <DU11>	A;Reference number: S22571; MUID:92020215; PMID:1923810	Qy	133 PRYEWTRTESTIWLTIVTDSDLAPSAAATDSPPRAGGLHAGVLEDGPGSSNGVLRPAAPG 72
A;Cross-references: UNIPROT:Q99MK3; UNIPARC:UPI000170BC8; EMBL:X60469; NID:957559; PID:NID:957559; PID:957559	A;Accession: S22571	Db	77 PSQGNSPPEQESQLTWTGP-----AHQGPFEGPFF---WKDEBEBAMEL--- 118
A;Status: nucleic acid sequence not shown; translation not shown	A;Molecule type: DNA	Qy	133 PRYEWTRTESTIWLTIVTDSDLAPSAAATDSPPRAGGLHAGVLEDGPGSSNGVLRPAAPG 72
A;Molecule type: DNA	A;Residues: 31-318 <DU12>	Db	77 PSQGNSPPEQESQLTWTGP-----AHQGPFEGPFF---WKDEBEBAMEL--- 118
A;Cross-references: UNIPARC:UPI000170BC9; EMBL:X60468; NID:957561; PID:CAA42998.1; PID:957561	A;Note: this sequence was submitted to the EMBL Data Library, July 1991	Qy	133 PRYEWTRTESTIWLTIVTDSDLAPSAAATDSPPRAGGLHAGVLEDGPGSSNGVLRPAAPG 72
C;Genetics:	C;Introns: 88/3; 107/3; 135/3; 157/3; 207/3; 250/2; 252/2; 290/3	Db	77 PSQGNSPPEQESQLTWTGP-----AHQGPFEGPFF---WKDEBEBAMEL--- 118
C;Keywords: transcription regulation	C;Keywords: transcription regulation	Qy	133 PRYEWTRTESTIWLTIVTDSDLAPSAAATDSPPRAGGLHAGVLEDGPGSSNGVLRPAAPG 72
F;42-78/Domain: WW repeat homology	F;42-78/Domain: WW repeat homology	Db	77 PSQGNSPPEQESQLTWTGP-----AHQGPFEGPFF---WKDEBEBAMEL--- 118
Query Match 9.8%; Score 75.5; DB 2; Length 499;	Best Local Similarity 25.6%; Pred. No. 29; Mismatches 59; Indels 23; Gaps 5;	Qy	133 PRYEWTRTESTIWLTIVTDSDLAPSAAATDSPPRAGGLHAGVLEDGPGSSNGVLRPAAPG 72
Matches 34; Conservative 17; Mismatches 59; Indels 23; Gaps 5;		Db	77 PSQGNSPPEQESQLTWTGP-----AHQGPFEGPFF---WKDEBEBAMEL--- 118

Search completed: May 20, 2006, 21:07:20
Job time : 40 SECs